

Mon Aug 30 08:48:58 2004

us-09-914-883-2.aug04.ra1

Page 1

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CM protein - protein search, using sw model

Run on: August 28, 2004, 04:05:25 ; Search time 23.1866 Seconds
(without alignments)
2195.179 Million cell updates/sec

Title: US-09-914-883-2
Perfect score: 5188
Sequence: 1 MALRRLGALLPLLAIVE.....ILNSIQWRAQWNIQISVEV 986

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 7

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 90%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

1:	/cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2:	/cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3:	/cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
4:	/cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
5:	/cgn2_6/ptodata/2/1aa/6C.COMB.pep.*
6:	/cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5130	98.9	994	3	US-08-542-635-2
2	5093	98.2	970	2	US-08-449-643A-11
3	5093	98.2	970	2	US-08-702-367A-11
4	5093	98.2	970	5	PCT-US95-04681-11
5	4993.5	95.3	995	1	US-08-162-809-18
6	4971.5	95.8	1011	1	US-08-162-809-12
7	4962.5	95.7	995	2	US-08-673-789-5

ALIGNMENTS

RESULT 1
US-08-542-635-2
; Sequence 2, Application US/08542635
; Patent No. 6218356
; GENERAL INFORMATION:
; APPLICANT: Pawson, Anthony
; APPLICANT: Henkemeyer, Mark
; APPLICANT: Letwin, Kenneth
; TITLE OF INVENTION: NOVEL NEURAL RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Betsekian & Parr
; STREET: 40 King Street West, Box 401
; CITY: Toronto

QY	10	LLLPPLAAVEETLMDSTATAELGMMVHPSPGMEVSGYDENMNTIRTYOVNPFESSQ	69
DB	18	LLLPPLAAVEETLMDSTATAELGMMVHPSPGMEVSGYDENMNTIRTYOVNPFESSQ	77
QY	70	NNMLRTFIRRCGRHRIHVEMKFSVDCSSIPSVPSCKETFMUYEADPDSATKTFPN	129
DB	78	NNMLRTFIRRCGRHRIHVEMKFSVDCSSIPSVPSCKETFMUYEADPDLATTFPN	137
QY	130	WMENPMVKVDITADESFQVDLGRVMKINTVRSFGVRSRGFYLAQDYGGCMLIA	189
DB	138	WMENPMVKVDITADESFQVDLGRVMKINTVRSFGVRSRGFYLAQDYGGCMLIA	197
QY	190	VRVYRRCPRITONGALFQETLSGAEISTLYAARGSCINAEVDPITLYCNGDEMLV	249
DB	198	VRVYRRCPRITONGALFQETLSGAEISTLYAARGSCINAEVDPITLYCNGDEMLV	257
QY	250	PICRCMKAGFEAVENGTVCRGCPGSGTFKANQDEACTHCPINRSTTSBQATNCVRNGY	309
DB	258	PICRCMKAGFEAVENGTVCRGCPGSGTFKANQDEACTHCPINRSTTSBQATNCVRNGY	317
QY	310	YRADLDPLDMPCTTIBAPQAVISSVAVETSLMELMTPRPSGREDLVNIIICKSGSGR	369
DB	318	YRADLDPLDMPCTTIBAPQAVISSVAVETSLMELMTPRPSGREDLVNIIICKSGSGR	377
QY	370	GACTRCGDNQVAPROGLTEPRITISDLIAHQYVFELIOAVNGVVDQSPFSPFASVNI	429
DB	378	GACTRCGDNQVAPROGLTEPRITISDLIAHQYVFELIOAVNGVVDQSPFSPFASVNI	437
QY	430	TTNOAASAVSINHQVSRITVDSITLSMSQPDQNGVILIDYELQYKEKLESEVATIKSP	489
DB	438	TTNOAASAVSINHQVSRITVDSITLSMSQPDQNGVILIDYELQYKEKLESEVATIKSP	497

QY 490 INTVTVOGKAGAIYVFOVRARTVAGYGRYSGKMYFQMTAEVQTSIOEKLPLIIGSSA 549
Db 498 INTVTVOGKAGAIYVFOVRARTVAGYGRYSGKMYFQMTAEVQTSIOEKLPLIIGSSA 557
QY 550 AGVLVLLVAVYAIYCNRRGFERADSEYTDKQHTSGHMPGKTIYIDPFTYEDPNEAV 609
Db 558 AGVLVLLVAVYAIYCNRRGFERADSEYTDKQHTSGHMPGKTIYIDPFTYEDPNEAV 617
QY 610 REFAPKIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIIFAIKTLKSGYTEKORRDFLS 669
Db 618 REFAPKIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIIFAIKTLKSGYTEKORRDFLS 677
QY 670 EASIMGQPDHPNVHLLEGVYTKSTPVMIIIFEMENGSLDSFLRQNDQGFYIQLVGMKRG 729
Db 678 EASIMGQPDHPNVHLLEGVYTKSTPVMIIIFEMENGSLDSFLRQNDQGFYIQLVGMKRG 737
QY 730 IAAKMYLADNMVYHRDLAARNILVNSLVCKVSDFGSLRLEDDTSDPTYSALGKIP 789
Db 738 IAAKMYLADNMVYHRDLAARNILVNSLVCKVSDFGSLRLEDDTSDPTYSALGKIP 797
QY 790 IRMTAPELQYRKRTSASDVWSYGIIVMEVMSYGERPYWMTNODVINAIEQDYRLPPEM 849
Db 798 IRMTAPELQYRKRTSASDVWSYGIIVMEVMSYGERPYWMTNODVINAIEQDYRLPPEM 857
QY 850 DCPBALHQLMDCQKXNRHPRKFGQIVNTLDKXIRPNLSIKAMAPLSSGINLPLDRTI 909
Db 858 DCPBALHQLMDCQKXNRHPRKFGQIVNTLDKXIRPNLSIKAMAPLSSGINLPLDRTI 917
QY 910 PDYTSFNTVDEWLEAIKXGQYKESFANAGFTSPDVVSQMMEDILRLGVTLAHOXKIIN 969
Db 918 PDYTSFNTVDEWLEAIKXGQYKESFANAGFTSPDVVSQMMEDILRLGVTLAHOXKIIN 977
QY 970 SIQVRAQNMQIQSVEV 986
Db 978 SIQVRAQNMQIQSVEV 994

RESULT 2
US-08-449-645A-11
Sequence 11, Application US/08449645A
Patent No. 5981245
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
NUMBER OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1840 Dehavenland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,645A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-449-645A-11

Query Match 98.2%; Score 5093; DB 2; Length 970;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 967; Conservative 2; Mismatches 1; Indels 2; Gaps 1;
QY 15 LAAVETLMDSTTATAEIGMMVHPSPSGMEESGYDENNNITRTYQVCFVSSQNNMLR 74
Db 1 LAAVETLMDSTTATAEIGMMVHPSPSGMEESGYDENNNITRTYQVCFVSSQNNMLR 60
QY 75 TKFIRRRGHRHVMKRSVRCSSIPSVPGSCRTNULYYEADFDATKTFPMWMEP 134
Db 61 TKFIRRRGHRHVMKRSVRCSSIPSVPGSCRTNULYYEADFDATKTFPMWMEP 120
QY 135 WKVVDITADESFSQVDLGRVMKINTEVRSFGPYRSRGFYAFODYGGCMSLIARVYF 194
Db 121 WKVVDITADESFSQVDLGRVMKINTEVRSFGPYRSRGFYAFODYGGCMSLIARVYF 180
QY 195 RKPRIIIONGALFQETLSGASTSIVARSGCIANAEEVDYPIKLXNGDGEWTVPIGR 254
Db 181 RKPRIIIONGALFQETLSGASTSIVARSGCIANAEEVDYPIKLXNGDGEWTVPIGR 240
QY 255 MCKAGFEAVENGTVRGCPGTFKANKQDEACTHCPIRSRTTSGATNCVCRNGYRADD 314
Db 241 MCKAGFEAVENGTVRGCPGTFKANKQDEACTHCPIRSRTTSGATNCVCRNGYRADD 300
QY 315 DPLMPCCTTISAPDAVISVNETSLMEWTTPPSDGGREDLVYNIICKSGSGRGACTR 374
Db 301 DPLMPCCTTISAPDAVISVNETSLMEWTTPPSDGGREDLVYNIICKSGSGRGACTR 360
QY 375 CGDNQVAPRQGLTEPRYISDLAHTQYFEEIQAVNGVTDGSPSPQFASVNTTNOA 434
Db 361 CGDNQVAPRQGLTEPRYISDLAHTQYFEEIQAVNGVTDGSPSPQFASVNTTNOA 420
QY 435 APSAVSIHQVSRVDSITLWSQPDQPNVYLDLQYKEKLESEYNATARKSPNTVT 494
Db 421 APSAVSIHQVSRVDSITLWSQPDQPNVYLDLQYKEKLESEYNATARKSPNTVT 480
QY 495 VOGKAGAIYVFOVRARTVAGYGRYSGKMYFQMTAEVQTSIOEKLPLIIGSSAALVF 554
Db 481 --GLKAGAIYVFOVRARTVAGYGRYSGKMYFQMTAEVQTSIOEKLPLIIGSSAALVF 538
QY 555 LIAVVVIAIYCNRRGFERADSEYTDKQHTSGHMPGKTIYIDPFTYEDPNEAVREFAK 614
Db 539 LIAVVVIAIYCNRRGFERADSEYTDKQHTSGHMPGKTIYIDPFTYEDPNEAVREFAK 598
QY 615 EIDISCVKTIQVIGAGEFGEVCSGHLKLPKREIIFAIKTLKSGYTEKORRDFLSASIM 674
Db 599 EIDISCVKTIQVIGAGEFGEVCSGHLKLPKREIIFAIKTLKSGYTEKORRDFLSASIM 658
QY 675 GQPDHPNVHLLEGVYTKSTPVMIIIFEMENGSLDSFLRQNDQGFYIQLVGMKRGIAAGM 734
Db 659 GQPDHPNVHLLEGVYTKSTPVMIIIFEMENGSLDSFLRQNDQGFYIQLVGMKRGIAAGM 718
QY 735 KYLADNMVYHRDLAARNILVNSLVCKVSDFGSLRLEDDTSDPTYSALGKIPIRMTA 794
Db 719 KYLADNMVYHRDLAARNILVNSLVCKVSDFGSLRLEDDTSDPTYSALGKIPIRMTA 778
QY 795 PEALQYRKFTSASDVWSYGIIVMEVMSYGERPYWMTNODVINAIEQDYRLPPEMCPBA 854
Db 779 PEALQYRKFTSASDVWSYGIIVMEVMSYGERPYWMTNODVINAIEQDYRLPPEMCPBA 838
QY 855 LHQLMDCQKXNRHPRKFGQIVNTLDKXIRPNLSIKAMAPLSSGINLPLDRTIPDYS 914
Db 839 LHQLMDCQKXNRHPRKFGQIVNTLDKXIRPNLSIKAMAPLSSGINLPLDRTIPDYS 898
QY 915 FNTVDEWLEAIKXGQYKESFANAGFTSPDVVSQMMEDILRLGVTLAHOXKIINSIQVM 974
Db 899 FNTVDEWLEAIKXGQYKESFANAGFTSPDVVSQMMEDILRLGVTLAHOXKIINSIQVM 958
QY 975 RAQMNQIQSVEV 986
Db 959 RAQMNQIQSVEV 970

RESULT 3

US-08-702-367A-11

Sequence 11, Application US/08702367A

Patent No. 5981246

GENERAL INFORMATION:

APPLICANT: Fox, Gary M.

TITLE OF INVENTION: Eph-like Receptor Protein Tyrosine

NUMBER OF INVENTION: Kinases

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Patent Operations/RBW

STREET: 1840 Dehavilland Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/702,367A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Winter, Robert B.

REFERENCE/DOCKET NUMBER: A-287

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 970 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-702-367A-11

Query Match 98.2%; Score 5093; DB 2; length 970;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 967; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

15 LLAAYETIMDSRTTAETAEIGMMVHPSPGWEESGYDENMNTTRTYOVQCNVFPSSQNMNLR 74
1 LLAAYETIMDSRTTAETAEIGMMVHPSPGWEESGYDENMNTTRTYOVQCNVFPSSQNMNLR 60
75 TKFIRRGARHIVHEKFSVRDCCSIPVPGSCKETFNLYYEADFDATKTFFPMWMEHP 134
61 TKFIRRGARHIVHEKFSVRDCCSIPVPGSCKETFNLYYEADFDATKTFFPMWMEHP 120
135 WKVVDITLADDESQVLDLGRVWKINTEVRSFGVSRSGFYAFQDYGCMSLIVRVFY 194
121 WKVVDITLADDESQVLDLGRVWKINTEVRSFGVSRSGFYAFQDYGCMSLIVRVFY 180
195 RKCPRIIOGALFQETLSGAESTSLVAARGSCIANAEVDVEIKLYCNDGEMLVPIGRG 254
181 RKCPRIIOGALFQETLSGAESTSLVAARGSCIANAEVDVEIKLYCNDGEMLVPIGRG 240
255 MCKAGEAVENGTVCGCGPSGTFTKANQGPDACTHCHINSRTTSEGATNCVANGNYIRADL 314
241 MCKAGEAVENGTVCGCGPSGTFTKANQGPDACTHCHINSRTTSEGATNCVANGNYIRADL 300
315 DPLDMCTTTPSPAPQVIVSVNETSIMLWTPPRDSCGREDVYVNIICKSCSGSGACTR 374
301 DPLDMCTTTPSPAPQVIVSVNETSIMLWTPPRDSCGREDVYVNIICKSCSGSGACTR 360
375 CGDNVQYAPRQGLTEPRRIYISDLAHQYTFEIQAVNGVTDOSPSPFASVNIITNOA 434
361 CGDNVQYAPRQGLTEPRRIYISDLAHQYTFEIQAVNGVTDOSPSPFASVNIITNOA 420
435 APSAVSIMQVSRIVTSITLWSQPOPOGVILDYELQYXKELSEYNATAIKSPNTVY 494
421 APSAVSIMQVSRIVTSITLWSQPOPOGVILDYELQYXKELSEYNATAIKSPNTVY 480

RESULT 4

PCT-US95-04681-11

Sequence 11, Application PC/TUS9504681

GENERAL INFORMATION:

APPLICANT: Fox, Gary M.

TITLE OF INVENTION: Eph-like Receptor Protein Tyrosine

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Patent Operations/RBW

STREET: 1840 Dehavilland Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04681

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Winter, Robert B.

REFERENCE/DOCKET NUMBER: A-287

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 970 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US95-04681-11

Query Match 98.2%; Score 5093; DB 5; length 970;

495 VQGLKAGAIYVQVARTVAGYGRYSCKYFQMTAEAYQTSIQEKLPIIGSSAAGLVF 554
481 --GLKAGAIYVQVARTVAGYGRYSCKYFQMTAEAYQTSIQEKLPIIGSSAAGLVF 538
555 LIAVVTIAIVCNRRGGERADSEYTDLQHTYSGHMPGKIYIDPPTYEDPNEAREFAK 614
539 LIAVVTIAIVCNRRGGERADSEYTDLQHTYSGHMPGKIYIDPPTYEDPNEAREFAK 598
615 EIDISCVKIEQVYAGFEGEVCSEHLKLPQKREIFVAIKTLKSGYTEKORPFLSEASIM 674
599 EIDISCVKIEQVYAGFEGEVCSEHLKLPQKREIFVAIKTLKSGYTEKORPFLSEASIM 658
675 GQFDHENVHLEGVVTKSTPVMITTEFMENGLSDFLRQNDQFTYIQVGMIRGIAAG 718
659 GQFDHENVHLEGVVTKSTPVMITTEFMENGLSDFLRQNDQFTYIQVGMIRGIAAG 718
735 KYLADNMVYHRLAARNILVNSNLVCKVSPGLSRFLEDOTSDPTYTSALGKIPIRMWA 794
719 KYLADNMVYHRLAARNILVNSNLVCKVSPGLSRFLEDOTSDPTYTSALGKIPIRMWA 778
795 PEAIQYRKFTSASDVMSYGIWMWVMSYGERPYWDMTNDVINAIEDYRLPPEMCPFA 854
779 PEAIQYRKFTSASDVMSYGIWMWVMSYGERPYWDMTNDVINAIEDYRLPPEMCPFA 838
855 LHQMLDQWQKDNHPRKFGQIVNTLDKMRNNSIKAMAPLSSGINLPILDRITPDYTS 914
839 LHQMLDQWQKDNHPRKFGQIVNTLDKMRNNSIKAMAPLSSGINLPILDRITPDYTS 898
915 FNTVDEWLLEAIKNGQYKESFANAGFTSFDVVSQMMEDILRVGVTLAEGKILNSIQVM 974
899 FNTVDEWLLEAIKNGQYKESFANAGFTSFDVVSQMMEDILRVGVTLAEGKILNSIQVM 958
975 RAQNMQIOSVEV 986
959 RAQNMQIOSVEV 970

Best Local Similarity 99.5%; Pred. No. 0;
Matches 967; Conservative 2; Mismatches 1; Indels 2; Gaps 1;
QY 15 LLAAVEETLMDSTATAELGMMVHPPSGMEVSGYDENMTITRYOVNVPESQNMWR 74
1 LLAAVEETLMDSTATAELGMMVHPPSGMEVSGYDENMTITRYOVNVPESQNMWR 60
QY 75 TKFTRRGARRIHYEMKFSYDCCSIPSPVSGCKETFNLYYYADPDSATKTPPMNENP 134
61 TKFTRRGARRIHYEMKFSYDCCSIPSPVSGCKETFNLYYYADPDSATKTPPMNENP 120
QY 135 WVKVDITAADESFQVDLGRVVKINTEVRSFGPVRSQGYLAFOYGGCMSLIARVRY 194
121 WVKVDITAADESFQVDLGRVVKINTEVRSFGPVRSQGYLAFOYGGCMSLIARVRY 180
QY 195 RKCPRITIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPKLYCNGDGEWLVPIGR 254
181 RKCPRITIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPKLYCNGDGEWLVPIGR 240
QY 255 MCKAGEAVENGTVCGCPGSGTFKANGDEACTHCHINSRTTSEGAATNCVNGGYRADL 314
241 MCKAGEAVENGTVCGCPGSGTFKANGDEACTHCHINSRTTSEGAATNCVNGGYRADL 300
QY 315 DPLDMPCTTIPSAPOAVISSVNETSLMLEWTPRDSGREDLVYNIICKSGSGRGACTR 374
301 DPLDMPCTTIPSAPOAVISSVNETSLMLEWTPRDSGREDLVYNIICKSGSGRGACTR 360
QY 375 CGDNVOYAPROGLTEPRITISDLAHTQYTFELQVNGVTQSPSPSPASVNTTQA 434
361 CGDNVOYAPROGLTEPRITISDLAHTQYTFELQVNGVTQSPSPSPASVNTTQA 420
QY 435 APSAVSIMQVSRVDSITLSWSQDPQNGVILDELYEYKELESEYNATAIKSPNTYT 494
421 APSAVSIMQVSRVDSITLSWSQDPQNGVILDELYEYKELESEYNATAIKSPNTYT 480
QY 495 VQGLKAGALIVQYRARTVAGYRSGKMYFQTMTEAEVQTSIOEKLPIITSSAAGLVF 554
481 -GLKAGALIVQYRARTVAGYRSGKMYFQTMTEAEVQTSIOEKLPIITSSAAGLVF 538
QY 555 LIAVVAIAIVCNRGFERADSEYTDLOHYTSGHMTGPKKIYIDFETVEDPNEAVREFAK 614
539 LIAVVAIAIVCNRGFERADSEYTDLOHYTSGHMTGPKKIYIDFETVEDPNEAVREFAK 598
QY 615 EIDISCVKIEOYIAGBEFGEVCSGHLKPGKREIFVAIKTLKSGYTEKQORDFLSEASIM 674
599 EIDISCVKIEOYIAGBEFGEVCSGHLKPGKREIFVAIKTLKSGYTEKQORDFLSEASIM 658
QY 675 GQFDHNVNTHLEGVYTKSTPVMIITEPMENGLDSFLRONDQGFVILQVGLRGLIAGM 734
659 GQFDHNVNTHLEGVYTKSTPVMIITEPMENGLDSFLRONDQGFVILQVGLRGLIAGM 718
QY 735 KTLADMNHYHRDLAARNILVNSNLVCKVDFGLSRFLEDDTSPTYSALGKPIRWTA 794
719 KTLADMNHYHRDLAARNILVNSNLVCKVDFGLSRFLEDDTSPTYSALGKPIRWTA 778
QY 795 PEAIQYRKFTASDVWSYGIWMEVMSYGERPYMNTNOVINAIEOYRILPRPNDGCSA 854
779 PEAIQYRKFTASDVWSYGIWMEVMSYGERPYMNTNOVINAIEOYRILPRPNDGCSA 838
QY 855 LHQMLDQCKXDRNRPKFGQIVNTLDKIRNPNSLKAMAPLSSGINPLDRTIPDYS 914
839 LHQMLDQCKXDRNRPKFGQIVNTLDKIRNPNSLKAMAPLSSGINPLDRTIPDYS 898
QY 915 KNTVEMEMLEATKMGYKESFANAGTSFDVVSQMMEDILKGLTILAHQKILNSIQVM 974
899 KNTVEMEMLEATKMGYKESFANAGTSFDVVSQMMEDILKGLTILAHQKILNSIQVM 958
QY 975 RAQMNOIQSVEV 986
958 RAQMNOIQSVEV 970

RESULT 5

US-08-162-809-18
Sequence 18, Application US/08162809
Patent No. 5457048
GENERAL INFORMATION:
APPLICANT: Pasquale, Elena B.
APPLICANT: Sajjadi, Fereydoon G.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NOCLEOTIDE SEQUENCES, AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 La Tolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States of America
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,809
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 995 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-162-809-18
Query Match 96.3%; Score 4993.5; DB 1; Length 995;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 937; Conservative 28; Mismatches 12; Indels 1; Gaps 1;
QY 10 LLLPLLAAVEETLMDSTATAELGMMVHPPSGMEVSGYDENMTITRYOVNVPESQ 69
18 LLLPLLAAVEETLMDSTATAELGMMVHPPSGMEVSGYDENMTITRYOVNVPESQ 77
QY 70 NMLRTKTYFIRRGARRIHYEMKFSYDCCSIPSPVSGCKETFNLYYYADPDSATKTPFN 129
78 NMLRTKTYFIRRGARRIHYEMKFSYDCCSIPSPVSGCKETFNLYYYADPDSATKTPFN 137
QY 130 MMENPMVKVDITAADESFQVDLGRVVKINTEVRSFGPVRSQGYLAFOYGGCMSLIAR 189
138 MMENPMVKVDITAADESFQVDLGRVVKINTEVRSFGPVRSQGYLAFOYGGCMSLIAR 197
QY 190 VRFVYRKCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPKLYCNGDGEWLV 249
198 VRFVYRKCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPKLYCNGDGEWLV 257
QY 250 PIRGCMCKAGFEVENGTVCRCGPGSGTFKANGDEACTHCHINSRTTSGAATNCVNGCY 309
258 PIRGCMCKAGFEVENGTVCRCGPGSGTFKANGDEACTHCHINSRTTSGAATNCVNGCY 317
QY 310 YRADLDPDMPCTTIPSAPOAVISSVNETSLMLEWTPRDSGREDLVYNIICKSGSGR 369
318 YRADLDPDMPCTTIPSAPOAVISSVNETSLMLEWTPRDSGREDLVYNIICKSGSGR 377
QY 370 GACTRCGDNVOYAPROGLTEPRITISDLAHTQYTFELQVNGVTQSPSPSPASVNTTQA 429
378 GACTRCGDNVOYAPROGLTEPRITISDLAHTQYTFELQVNGVTQSPSPSPASVNTTQA 437
QY 430 TTNOAPASVAVSIMQVSRVDSITLSWSQDPQNGVILDELYEYKELESEYNATAIKSP 489

Mon Aug 30 08:48:58 2004

us-09-914-883-2.aug04.ra1

Page 5

Db 438 TTNQAPSAVSIMQVSRVDSITLSMSQDPDPNGVITLDELYQYEKINSELNSTAVNSP 497
Qy 490 TINTVVOGLKAGAIYVQVARTVAGYGRYSGRMVFOQMTBAEYQTSIOEKLPLIGSSA 549
Db 498 TINTVVOGLKAGAIYVQVARTVAGYGRYSGRMVFOQMTBAEYQTSIOEKLPLIGSSA 557
Qy 550 AGVFLIAVVVIAIVCN-RGFEERADSEYTDKLOHTYSGHMPGKIYIDPFTYEDPNEA 608
Db 558 AGVFLIAVVVIAIVCNRRRGERADSEYTDKLOHTYSGHMPGKIYIDPFTYEDPNEA 617
Qy 609 VEEFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIIFAIKTLKSGYTEKORRDFL 668
Db 618 VEEFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIIFAIKTLKSGYTEKORRDFL 677
Qy 669 SEASITGQDPHNVTHLEGVVTKSTPVMITTEPMENGLDSFLKQNDGQFTVYQLVGMLR 728
Db 678 SEASITGQDPHNVTHLEGVVTKSTPVMITTEPMENGLDSFLKQNDGQFTVYQLVGMLR 737
Qy 729 GIAAGKYLADMYVVRDLAARNILVNSLVCKVSDPGLSRFLEDDPTSDPTYSALGSKI 788
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Db 798 PIRWTAPEALIQYRKFTSASDVWSYGIVMWEVNSYGERPYWMTNODVINALBQDYRLPPP 857
Qy 849 MDCPSALHQLMDCMQKDRNRHPRFGQIVNTLDKMIKRNPNLSLKAPLSSGGINFLDLRT 908
Db 858 MDCPSALHQLMDCMQKDRNRHPRFGQIVNTLDKMIKRNPNLSLKAPLSSGGINFLDLRT 917
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Db 918 IDFTYSFNTVDEMLBAIKMGQYKESFASAGFTTFPDIVSQMTVEDILRQVTLAIGHQKIL 977
Qy 969 NSIQVRAQMNQIQSYEV 986
Db 978 NSIQVRAQMNQIQSYEV 995

RESULT 6
US-08-162-809-112
Sequence 12, Application US/08162809
Patent No. 5457048
GENERAL INFORMATION:
APPLICANT: Pasquale, Elena B.
APPLICANT: Sajjadi, Fereydoon G.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States of America
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162, 809
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949

Qy 10 LLLPLAAVEETMDSTTAELGMMVHPSPGMEVEYSYDENMNTIRTYQVNCVFRSSQ 69
Db 18 LALPLAAVEETMDSTTAELGMMVHPSPGMEVEYSYDENMNTIRTYQVNCVFRSSQ 77
Qy 70 NNMWRTKFIIRRGARHRIHVENKFSVRDCSSI PSYVSGCKETFNLYYEADPDSATKTFPN 129
Db 78 NNMWRTKFIIRRGARHRIHVENKFSVRDCSSI PSYVSGCKETFNLYYEADPDSATKTFPN 137
Qy 130 MMENPMYKVDITLADSEFSQVDLGGRYMKINTEVRSFGPVSRSQGFYLAPODYGCNSLIA 189
Db 138 MMENPMYKVDITLADSEFSQVDLGGRYMKINTEVRSFGPVSRSQGFYLAPODYGCNSLIA 197
Qy 190 VRFVYRRCPRILIONGALFOETLSGAEISTSLVAARGSCIANAEVVDVBIKLYCNGDGEMLV 249
Db 198 VRFVYRRCPRILIONGALFOETLSGAEISTSLVAARGSCIANAEVVDVBIKLYCNGDGEMLV 257
Qy 250 PIRGCMKAGFEAVENVTGRCGSPGFEXANOGDEACTHCPINSRTSBEATNOCVNGY 309
Db 258 PIRGCMKAGFEAVENVTGRCGSPGFEXANOGDEACTHCPINSRTSBEATNOCVNGY 317
Qy 310 YRADLDELMECTTIPAPQAVISSVNETSLMEWTPRPSGREDLVYNIICKSCSGSR 369
Db 318 YRADLDELMECTTIPAPQAVISSVNETSLMEWTPRPSGREDLVYNIICKSCSGSR 377
Qy 370 GACTRCGDNQVAPRQGLTEPRYISDLAHTOYTFEIOAVNGVTDQSPSPFASVNI 429
Db 378 GACTRCGDNQVAPRQGLTEPRYISDLAHTOYTFEIOAVNGVTDQSPSPFASVNI 437
Qy 430 TTNQAPSAVSIMQVSRVDSITLSMSQDPDPNGVITLDELYQYEKINSELNSTAVNSP 489
Db 438 TTNQAPSAVSIMQVSRVDSITLSMSQDPDPNGVITLDELYQYEKINSELNSTAVNSP 497
Qy 490 TINTVVOGLKAGAIYVQVARTVAGYGRYSGRMVFOQMTBAEYQTSIOEKLPLIGSSA 549
Db 498 TINTVVOGLKAGAIYVQVARTVAGYGRYSGRMVFOQMTBAEYQTSIOEKLPLIGSSA 557
Qy 550 AGVFLIAVVVIAIVCN-RGFEERADSEYTDKLOHTYSGHMPGKIYIDPFTYEDPNEA 608
Db 558 AGVFLIAVVVIAIVCNRRRGERADSEYTDKLOHTYSGHMPGKIYIDPFTYEDPNEA 617
Qy 593 MKIYIDPFTYEDPNEA VEEFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIIFA 652
Db 618 MKIYIDPFTYEDPNEA VEEFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIIFA 677
Qy 653 KTLKSGYTEKORRDFLSEASITGQDPHNVTHLEGVVTKSTPVMITTEPMENGLDSFLR 712
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Qy 713 QNDGQFTVYQLVGMLRGIAGMKYLADMYVVRDLAARNILVNSLVCKVSDPGLSRFLE 772
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Qy 773 DQTSDDPTYSALGSKIPIRWTAPALIOYRKFTSASDVWSYGIVMWEVNSYGERPYWMTN 832
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Qy 833 QDVNNAIEODYRLPPPDCRNALHQLMDCMQKDRNRHPRFGQIVNTLDKMIKRNPNLSLK 892
Db 858 QDVNNAIEODYRLPPPDCRNALHQLMDCMQKDRNRHPRFGQIVNTLDKMIKRNPNLSLK 917
Qy 893 MAPUSSGINPLDLRTIPDYTSFNTVDEMLBAIKMGQYKESFANAGFTSFVVSQMMED 952

DB 918 MALLSSGVNPLDRLTPTDTSFNTVDENMLDAIKMSQYKESFASAGFTTFDVSQMTVED 977

QY 953 ILRLGVTLAGHOKKILNSIQVMRAQMNQIOSVEV 986

DB 978 ILRVGVTLAGHOKKILNSIQVMRAQMNQIOSVEV 1011

RESULT 7

US-08-673-789-5

Sequence 5, Application US/08673789

Patent No. 5814479

GENERAL INFORMATION:

APPLICANT: ZHOU, RENPING; SCHULZ, NICHOLAS,

APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOUDE,

APPLICANT: GEORGE, F.

TITLE OF INVENTION: BSK RECEPTOR LIKE

TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AND THEIR

TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/673,789

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/177,812

FILING DATE: 04-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPEI

REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4105

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEFAX: (212) 751-6849

TELEX: 421792

INFORMATION FOR SEQ. ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 995

TYPE: AMINO ACID

STRANDEDNESS: UNKNOWN

TOPOLOGY: UNKNOWN

US-08-673-789-5

Query Match 95.7%; Score 4962.5; DB 2; Length 995;

Best Local Similarity 95.1%; Pred. No. 0;

Matches 930; Conservative 30; Mismatches 17; Indels 1; Gaps 1;

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DB 18 LALLPLLAAVEETLMDSTATAELGWMVHPGSGWEVSGYDENMNTIRTYQVCNFESSQ 77

QY 70 NMLRTKFIARRRGAHIIHVMKFSVVDGSSIPVPSGCKETNLIYYEADPFSATKTFPN 129

DB 78 NMLRTKFIARRRGAHIIHVMKFSVVDGSSIPVPSGCKETNLIYYEADPFSATKTFPN 137

QY 130 WKENPVKVDITLAADSFQVDLGGVWMIKINTEVRSFGVSRSGFYLAFODYGGCMSLIA 189

DB 138 WKENPMKVDITLAADSFQVDLGGVWMIKINTEVRSFGVSRSGFYLAFODYGGCMSLIA 197

QY 190 VRVFYKCRITIQNGAIFQETLSGAESTSLVAARGSCTIANAEVDVPIKLYCNGDEWLV 249

DB 198 VRVFYKCRITIQNGAIFQETLSGAESTSLVAARGSCTIANAEVDVPIKLYCNGDEWLV 257

QY 250 PIGRCMKAGEAVENGTVRCGCPSGTFKANOGDEACTHCPINSRTSSECATNCVCRNGY 309

DB 258 PIGRCMKRPGVESYENGTVCRCGCPSGTFKASQDEGCVHCPINSRTSSECATNCVCRNGY 317

QY 310 YRADLPDLMPCCTTIPAPAVISSVNETSLMELMTPRDSGREDLVNIIICKSGSGR 369

DB 318 YRADLPDLMPCCTTIPAPAVISSVNETSLMELMTPRDSGREDLVNIIICKSGSGR 377

QY 370 GACTRCGDNDQVAPRQGLTEPRITISDLAHTQYFEIQAIVGVTDQSPFSQFASVNI 429

DB 378 GACTRCGDNDQVAPRQGLTEPRITISDLAHTQYFEIQAIVGVTDQSPFSQFASVNI 437

QY 430 TTNOAASAVSINHQSRTVDSITLSNSQPDQNGVILDELOYEKEKSEYNATAIKSP 489

DB 438 TTNOAASAVSINHQSRTVDSITLSNSQPDQNGVILDELOYEKEKSEYNATAIKSP 497

QY 490 TINTVQGLKAGAIYVQVARTVAGYGRSGKRYQIMTEAEYQTSICRKLPLIIGSSA 549

DB 498 TINTVQGLKAGAIYVQVARTVAGYGRSGKRYQIMTEAEYQTSICRKLPLIIGSSA 557

QY 550 AGVFLIAVVAIVCN-RGFERADSEYTDKLQHTYSGHMPQMKIYIDPFYEDPNEA 608

DB 558 AGVFLIAVVAIVCN-RGFERADSEYTDKLQHTYSGHMPQMKIYIDPFYEDPNEA 617

QY 609 VREFAKEDISCVKIEQVIGAGEFEGVCSGHLPGKREIFVAIKTLKSGYTEKORRDFI 668

DB 618 VREFAKEDISCVKIEQVIGAGEFEGVCSGHLPGKREIFVAIKTLKSGYTEKORRDFI 677

QY 669 SEASIMQFDPHPNVIIHLEGVYTKSTPVMITTEPMENGSIDSFURQNDQGFVIQIVGMUR 728

DB 678 SEASIMQFDPHPNVIIHLEGVYTKSTPVMITTEPMENGSIDSFURQNDQGFVIQIVGMUR 737

QY 729 GIAQMKYLDMMYVHRDLAARNILVNSNLVCVSPFGSLFLEDDTSDPTYSALGKI 788

DB 738 GIAQMKYLDMMYVHRDLAARNILVNSNLVCVSPFGSLFLEDDTSDPTYSALGKI 797

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DB 798 PIRWTAPBEAIOYRKFTSASDWSYGIWMEVMSYGERPYWDMTNOQVINAIEQDYRLPP 857

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DB 858 MDCPSALHQLMDCWQDRVHRPKFGQIVNTLDKMTIRNPISLKAMPPLSSGINTPLDRT 917

QY 909 IPDYTSFNTVDENMLDAIKMSQYKESFASAGFTTFDVSQMTVEDILRVGVTLAGHOKKIL 968

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QY 969 NSIQVMRAQMNQIOSVEV 986

DB 978 NSIQVMRAQMNQIOSVEV 995

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Job time : 26.1886 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2004, 04:08:55 ; Search time 62.8025 Seconds
(without alignments)
4939.422 Million cell updates/sec

Title: US-09-914-883-2
Perfect score: 5188
Sequence: 1 MALRRIGALLLLPLLAWE.....INSIQWRAQWNCIQSEV 986

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 3

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 90%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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 - 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5181	99.9	1055	US-10-648-593-139	Sequence 139, App
2	5171.5	99.7	987	US-10-295-027-1193	Sequence 1193, Ap
3	4993.5	96.3	995	US-10-029-020-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1
US-10-648-593-139
; Sequence 139, Application US/10648593
; Publication No. US20040106132A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT

TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
FILE REFERENCE: D0273 NP
CURRENT APPLICATION NUMBER: US/10/648,593
CURRENT FILING DATE: 2003-08-26
PRIOR APPLICATION NUMBER: 60/406,385
PRIOR FILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 557
SOFTWARE: PatentIn version 3.2
SEQ ID NO 139
LENGTH: 1055
TYPE: PRT
ORGANISM: Homo sapiens
US-10-648-593-139

Query Match 99.9% Score 5181; DB 16; Length 1055;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 984; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB	1	MALRRIGALLLLPLLAWEETLMDSTTATLGMVHPSPGWEVSGYDENMTIRTYQ	60
QY	61	VCNVFESSQNNWLTKEIRRGARHIVENKFSYDCCSIPSVGSCKEFTNLYYEADF	120
DB	61	VCNVFESSQNNWLTKEIRRGARHIVENKFSYDCCSIPSVGSCKEFTNLYYEADF	120
QY	121	DSATKTFNNMENNWVVDITAADESFOYDLGGVKKINEVSPFVSASGTYLAFOD	180
DB	121	DSATKTFNNMENNWVVDITAADESFOYDLGGVKKINEVSPFVSASGTYLAFOD	180
QY	181	YGGCMSLIAVAVFYKCPRIIIONGAIQETLSGAESTSLVAARSCIANAEVDPILKY	240
DB	181	YGGCMSLIAVAVFYKCPRIIIONGAIQETLSGAESTSLVAARSCIANAEVDPILKY	240
QY	241	CNGGEMLVPIGRCMCAFEAVENGTCVCGPSTGKANOGDACHPCINSTTSEGA	300
DB	241	CNGGEMLVPIGRCMCAFEAVENGTCVCGPSTGKANOGDACHPCINSTTSEGA	300
QY	301	TNCVCRNGYRADLPDMPCTTIPSAPOAVISSVNETSLMLEWTPRDSGGREDLYNI	360
DB	301	TNCVCRNGYRADLPDMPCTTIPSAPOAVISSVNETSLMLEWTPRDSGGREDLYNI	360
QY	361	ICKCGSGRGACRCCGNVQVAPQQLTEPRITISDLAHTQYTFEIOAVNGYTDSPF	420
DB	361	ICKCGSGRGACRCCGNVQVAPQQLTEPRITISDLAHTQYTFEIOAVNGYTDSPF	420
QY	421	SPQASVNTITNQAAPSAVSIMHVSRTVDSITLSWQPOQPNVILDEYEOYEKLS	480
DB	421	SPQASVNTITNQAAPSAVSIMHVSRTVDSITLSWQPOQPNVILDEYEOYEKLS	480
QY	481	YNATPAIKSPNTVTVOGLKAGAIYFOVRAPTYAGYRGYSGKMPQMTBAEYOTSIOEK	540
DB	481	YNATPAIKSPNTVTVOGLKAGAIYFOVRAPTYAGYRGYSGKMPQMTBAEYOTSIOEK	540
QY	541	LPLITGSSAAGLVLLIAVVIATVCNRGFERDSEYTDLOHTSGHMPGKIYIDPF	600
DB	541	LPLITGSSAAGLVLLIAVVIATVCNRGFERDSEYTDLOHTSGHMPGKIYIDPF	600
QY	601	TYEDPNEAVBEFAKEIDISCVKIEQVIGAGEFEGVCSGHLKPKREI FVAIKTLKSGYT	660
DB	601	TYEDPNEAVBEFAKEIDISCVKIEQVIGAGEFEGVCSGHLKPKREI FVAIKTLKSGYT	660
QY	661	EKQRDLSEASIMGQDPHNVIHLGAVTKSPVMTTEFPMNGSIDSLRQNDQFTV	720
DB	661	EKQRDLSEASIMGQDPHNVIHLGAVTKSPVMTTEFPMNGSIDSLRQNDQFTV	720
QY	721	IQLVGMRLGIAAGKYLADNNVYHRDLAENILVNSNLVCVSDFGLSRFLLEDTSPTY	780
DB	721	IQLVGMRLGIAAGKYLADNNVYHRDLAENILVNSNLVCVSDFGLSRFLLEDTSPTY	780
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Db      781  TSALGKIPRMTAPEAIQYRKFTSADVWSYGI VMMWEVMSYGERPYMDNTQDVINAIE 840
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      841  QDRLEPPMDCCPSALHQLMLDCWQKDRNRPKRGQIVNTLDKXIRPNLSLKMAPLSSGI 900
QY      901  INLEPLDRITPDYTSFNTVDSEMLEAIKMGQYKESFANAGFTSPDVVSQMMEDILRLGYTL 960
      901  INLEPLDRITPDYTSFNTVDSEMLEAIKMGQYKESFANAGFTSPDVVSQMMEDILRLGYTL 960
Db      961  AGHOKKILNSIQYMRQAQNNQIOSVE 985
QY      961  AGHOKKILNSIQYMRQAQNNQIOSVE 985
      961  AGHOKKILNSIQYMRQAQNNQIOSVE 985
Db      961  AGHOKKILNSIQYMRQAQNNQIOSVE 985

RESULT 2
US-10-295-027-1193
; Sequence 1193, Application US/10295027
; Publication No. US200302350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295, 027
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663, 733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350, 666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335, 394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332, 464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334, 393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340, 376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347, 211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347, 349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355, 250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356, 714
; PRIOR FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: US 60/356, 714
; REMAINING PRIOR APPLICATION data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 1193
; LENGTH: 987
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-1193

Query Match      99.7%; Score 5171.5; DB 15; Length 987;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 984; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

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QY      121  DSAITKPEPMNENPWWVVDITIADESFSQYDLGRWVKITEVRSFPGVSAFGYLAFOD 180
      121  DSAITKPEPMNENPWWVVDITIADESFSQYDLGRWVKITEVRSFPGVSAFGYLAFOD 180
      121  DSAITKPEPMNENPWWVVDITIADESFSQYDLGRWVKITEVRSFPGVSAFGYLAFOD 180
QY      181  YGCGMSLIAVRVFPKCPRIIIONGAIFQETLSGAESTSLVAAGSCCIANAEEVDVPIKLY 240
      181  YGCGMSLIAVRVFPKCPRIIIONGAIFQETLSGAESTSLVAAGSCCIANAEEVDVPIKLY 240
      181  YGCGMSLIAVRVFPKCPRIIIONGAIFQETLSGAESTSLVAAGSCCIANAEEVDVPIKLY 240
Db      241  CNGDGEWLVPIIGCMCKAGFEAVENGTVCGCGSGGTFKAGQGBACTHCPINSRTSEGA 300
      241  CNGDGEWLVPIIGCMCKAGFEAVENGTVCGCGSGGTFKAGQGBACTHCPINSRTSEGA 300
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QY      301  TNCVCNNGYRADLDPDMECTTIPSAQAVISSVNETSLMBTPPDRSGGEEDLVYNI 360
      301  TNCVCNNGYRADLDPDMECTTIPSAQAVISSVNETSLMBTPPDRSGGEEDLVYNI 360
      301  TNCVCNNGYRADLDPDMECTTIPSAQAVISSVNETSLMBTPPDRSGGEEDLVYNI 360
QY      361  ICKSCGSGRACTRCGNNNOYAPRQLGLTEPRYISDLAHQYTEIQAQVNVQOSPF 420
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      361  ICKSCGSGRACTRCGNNNOYAPRQLGLTEPRYISDLAHQYTEIQAQVNVQOSPF 420
QY      421  SPQFASVNIITNQAPAPSAVSIHQVSRVDSITLSWQDPQNGVILLDELYEKEKELSE 480
      421  SPQFASVNIITNQAPAPSAVSIHQVSRVDSITLSWQDPQNGVILLDELYEKEKELSE 480
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QY      481  YNATAIKSPNTVTVQGLKAGALYVFPYRARTAGYGRYSGKMYFQMTAEVQTSIQEK 540
      481  YNATAIKSPNTVTVQGLKAGALYVFPYRARTAGYGRYSGKMYFQMTAEVQTSIQEK 540
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QY      541  LPLIIGSSAAGLVPLIAVVIATVCN-RGFERADSEYTDKLOHYTSGHMTPMKTIYIDP 599
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QY      841  EQDYRLPMPMDCCPSALHQLMLDCWQKDRNRPKRGQIVNTLDKXIRPNLSLKMAPLSSG 900
      841  EQDYRLPMPMDCCPSALHQLMLDCWQKDRNRPKRGQIVNTLDKXIRPNLSLKMAPLSSG 900
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QY      900  INLEPLDRITPDYTSFNTVDSEMLEAIKMGQYKESFANAGFTSPDVVSQMMEDILRLGYT 959
      900  INLEPLDRITPDYTSFNTVDSEMLEAIKMGQYKESFANAGFTSPDVVSQMMEDILRLGYT 959
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QY      960  LAGHOKKILNSIQYMRQAQNNQIOSVEV 986
      960  LAGHOKKILNSIQYMRQAQNNQIOSVEV 986
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QY      961  LAGHOKKILNSIQYMRQAQNNQIOSVEV 987
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RESULT 3
US-10-029-020-62
; Sequence 62, Application US/10029020
; Publication No. US2004003971A1
; GENERAL INFORMATION:
; APPLICANT: Gansoili et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/10/029, 020

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Mon Aug 30 08:48:58 2004

us-09-914-883-2.aug04.rapb

Page 3

;; CURRENT FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 60/256,704
;; PRIOR FILING DATE: 2000-12-19
;; PRIOR APPLICATION NUMBER: 60/311,590
;; PRIOR FILING DATE: 2001-08-10
;; PRIOR APPLICATION NUMBER: 60/257,314
;; PRIOR FILING DATE: 2000-12-20
;; PRIOR APPLICATION NUMBER: 60/311,613
;; PRIOR FILING DATE: 2001-08-10
;; PRIOR APPLICATION NUMBER: 60/315,617
;; PRIOR FILING DATE: 2001-08-29
;; PRIOR APPLICATION NUMBER: 60/307,506
;; PRIOR FILING DATE: 2001-07-24
;; PRIOR APPLICATION NUMBER: 60/322,358
;; PRIOR FILING DATE: 2001-09-14
;; PRIOR APPLICATION NUMBER: 60/294,075
;; PRIOR FILING DATE: 2001-05-29
;; PRIOR APPLICATION NUMBER: 60/288,153
;; PRIOR FILING DATE: 2001-05-02
;; NUMBER OF SEQ ID NOS: 190
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 62
;; LENGTH: 995
;; TYPE: PRT
;; ORGANISM: Gallus gallus
US-10-029-020-62

Query Match 96.3%; Score 4993.5; DB 12; Length 995;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 937; Conservative 28; Mismatches 12; Indels 1; Gaps 1;

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DB 18 LALLPLPLAAVEETIMDSTATAELGMMVHPPGSGMEVSGYDENMTIRTYQVCONVFESSQ 77
QY 70 NNMFLRTKFIIRRGARHIEHMKFSVDCSIPSPSSCKETPLIYYEADFDSATKTFPN 129
DB 78 NNMFLRTKFIIRRGARHIEHMKFSVDCSIPSPSSCKETPLIYYEADFDSATKTFPN 137
QY 130 WMENPMVKVDTIADSSFSQVDLGRVMKINTEVRSGFVPSRSGFYLAFOYGGCWSLIA 189
DB 138 WMENPMVKVDTIADSSFSQVDLGRVMKINTEVRSGFVPSRSGFYLAFOYGGCWSLIA 197
QY 190 VRFVYRKCPRITIONGAIPOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEMLV 249
DB 198 VRFVYRKCPRITIONGAIPOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEMLV 257
QY 250 PIGRCCKAGFEAVENGTVCRGCPGTFNANOGDEACTCPINSRTTSGATNCVCRRNGY 309
DB 258 PIGRCCKAGFEAVENGTVCRGCPGTFNANOGDEACTCPINSRTTSGATNCVCRRNGY 317
QY 310 YRADLDPLMDPCTTIPSAPOAVTSSVNETSLMLEWTPPRDSGREDLVYNIICKSCGSGR 369
DB 318 YRADLDPLMDPCTTIPSAPOAVTSSVNETSLMLEWTPPRDSGREDLVYNIICKSCGSGR 377
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DB 378 GACTRCGDNVQVAPROLGTEPRITISDLAHTQVFEIQAUNGVTDOSPPSPQFASVNI 437
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QY 550 AGLVFLAIVVIAIVGN-RRGFERADESEYDKLQHTSGHMTPGMKIYIDPFYEDPNEA 608
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QY 609 VREFPAKEIDISCVKIEQVIGAGFEFVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDFL 668

DB 618 VREFPAKEIDISCVKIEQVIGAGFEFVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDFL 677
QY 669 SEASIMGQFDHPNVIIHLEGVVTASTPYMTITEEMENSGSLSPFLQNDQGFVIOLVGMRL 728
DB 678 SEASIMGQFDHPNVIIHLEGVVTASTPYMTITEEMENSGSLSPFLQNDQGFVIOLVGMRL 737
QY 729 GIAAGMKYIADNMYVHRDLAARNILVNSNYCKVSDFGLSRFLBDDPTSDPTYSALGKXI 788
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QY 789 PIRWTAPPAIOYRKFTSASDVMSYGIWMEVMSYGERPPYMDMTNODVYINAIEQDYLPP 848
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DB 918 IPDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFVVSQMMEDILRLGVTLAGHQKIL 977
QY 969 NSIQVMRAQNNQIOSVEY 986
DB 978 NSIQVMRAQNNQIOSVEY 995

Search completed: August 28, 2004, 04:17:14
Job time : 63.8025 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2004, 03:50:54 ; Search time 18.3577 Seconds
(without alignments)
2736.715 Million cell updates/sec

Title: US-09-914-883-2
Perfect score: 5188
Sequence: 1 MALRRLGALLPLPLAAVE.....LINSIQVMRAQNMQIQSYEV 986

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 90%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB	ID Description
1	5184	99.9	1055 1 EPH2 HUMAN P29323 homo sapien
2	5130	98.9	1994 1 EPH2 MOUSE P54763 mus musculu
3	4975.5	95.9	1004 1 EPH2 CHICK P28693 gallus gall
4	4945	95.3	987 1 EPH2 COTUA Q90344 coturnix co

ALIGNMENTS

RESULT 1
EPH2_HUMAN STANDARD; PRT; 1055 AA.
ID EPH2_HUMAN
AC P29323; O43477;
DT 01-DEC-1992 (Rel. 24, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ephrin type-B receptor 2 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor EPH-3) (DRT) (Receptor protein-tyrosine kinase HK5) (ERK).
GN EPHB2 OR EPH3 OR ERK OR DRT OR HK5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
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RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RC TISSUE=Fetal brain;
RA Iregaki N., Tang X.X., Liu X.-G., Siegel J.A., Allen C., Yoshioaka A., Sultan E.P., Brodeur G.M., Pleasure D.B.;
RT "Molecular characterization and chromosomal localization of DRT (EPH3): a developmentally regulated human protein-tyrosine kinase gene of the EPH family.";

RL Hum. Mol. Genet. 4:2033-2045(1995).
RP [2]
RC SEQUENCE FROM N.A. (ISOFORM SHORT).
RC TISSUE=Gastric carcinoma;
RX MEDLINE=93343925; PubMed=7688222;
RA Iwase T., Tanaka M., Suzuki M., Naito Y., Sugimura H., Kino I.;
RT "Identification of protein-tyrosine kinase genes preferentially expressed in embryo stomach and gastric cancer.";
RL Biochem. Biophys. Res. Commun. 194:698-705(1993).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RC TISSUE=Fetal brain;
RX MEDLINE=98359217; PubMed=9696046;
RA Tang X.X., Pleasure D.B., Brodeur G.M., Iregaki N.;
RT "A variant transcript encoding an isoform of the human protein tyrosine kinase EPHB2 is generated by alternative splicing and alternative use of polyadenylation signals.";
RL Oncogene 17:521-526(1998).
RN [4]
RP SEQUENCE OF 15-986 FROM N.A. (ISOFORM SHORT).
RC TISSUE=Brain;
RX MEDLINE=95206782; PubMed=7898931;
RA Fox G.M., Holst P.L., Chute H.T., Lindberg R.A., Janssen A.M., Baeu R., Welcher A.A.;
RT "cDNA cloning and tissue distribution of five human EPH-like receptor protein-tyrosine kinases.";
RL Oncogene 10:897-905(1995).
RN [5]
RP SEQUENCE OF 509-986 FROM N.A. (ISOFORM SHORT).
RC TISSUE=Brain;
RA Saito T., Naohiko S., Kitahara M., Murata M., Yamamoto Y., Hori T., Matsuda Y.;
RT Submitted (Aug-1994) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 652-712 FROM N.A.
RX MEDLINE=91296384; PubMed=1648701;
RA Chan J., Watt V.M.;
RT "eek and erk, new members of the eph subclass of receptor protein-tyrosine kinases.";
RL Oncogene 6:1057-1061(1991).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) OF 910-986 (ISOFORM SHORT).
RX MEDLINE=99132419; PubMed=9933164;
RA Thanas C.D., Goodwill K.E., Bowie J.U.;
RT "Oligomeric structure of the human EphB2 receptor SAM domain.";
RL Science 283:833-836(1999).
CC -1- FUNCTION: Receptor for members of the ephrin-B family.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
CC -1- SUBUNIT: The ligand-activated form interacts with multiple proteins, including GRASP-activating protein (RASGAP) through its SH2 domain. Binds RASGAP through the juxtamembrane tyrosines residues. Interacts with PRKCBP (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named Isoforms=2;
CC Name=Long; Synonyms=EPHB2V;
CC IsoId=P29323-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=P29323-2; Sequence=VSP_003016, VSP_003017;
CC -1- TISSUE SPECIFICITY: Brain, heart, lung, kidney, placenta, pancreas, liver and skeletal muscle. Preferentially expressed in fetal brain.
CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin receptor subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is retained. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL; L41939; AAA93910.1; -
DR EMBL; D31661; BAA06506.1; -
DR EMBL; AF025304; AAB94602.1; -
DR EMBL; D14717; BAA03537.1; -
DR EMBL; L36643; AAA74244.1; -
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DR EMBL; X59292; CAA41981.1; -
DR PIR; A57174; A57174.
DR PDB; 1B4F; 16-FEB-99.
DR PDB; 1FOM; 04-JUL-00.
DR Genew; HGNC:3393; EPHB2.
DR MIM; 600997; -
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005005; F:transmembrane-ephrin receptor activity; TAS.
DR GO; GO:0007399; P:neurogenesis; TAS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR001090; Ephrin_receptor.
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DR InterPro; IPR003961; FN_III_subd.
DR InterPro; IPR008978; Gal_bind_like.
DR InterPro; IPR007719; Prot_kinase.
DR InterPro; IPR001660; SAM.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR InterPro; IPR001426; YKase_receptorV.
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DR PRINTS; PR00109; TYRKINASE.
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DR Prodom; PD000001; Prot_kinase; 1.
DR SMART; SM00615; Epp_1bd; 1.
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DR PROSITE; PS01186; EGF_2; UNKNOWN 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS5011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PS50105; SAM_DOMAIN; 1.
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KM Receptor; Transmembrane; Glycoprotein; Signal; 3D-structure;
KM Alternative splicing; Repeat.
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FT DOMAIN 19 543
FT TRANSMEM 544 564
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FT BINDING 653 653
FT ACT_SITE 746 746
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Missing (in isoform Short).
/FTId=VSP_003017.
A->R.
/FTId=VAR_004162.
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(IN REF. 2).
G->D (IN REF. 2).
K->KQ (IN REF. 2).
MISSING (IN REF. 4).
E->D (IN REF. 2).
R->RR (IN REF. 1).
M->I (IN REF. 4).
I->F (IN REF. 2 AND 5).
S->A (IN REF. 2 AND 5).
E->K (IN REF. 2 AND 5).
L->V (IN REF. 3).
V->L (IN REF. 1).

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QY 541 LPLIIGSSAAGLVFLLIAVVAIVACNRRGFERADSEYTKLQHTYSGHMTPGKIKYIDPF 600
DB 541 LPLIIGSSAAGLVFLLIAVVAIVACNRRGFERADSEYTKLQHTYSGHMTPGKIKYIDPF 600
QY 601 TYDDPNEANREPKEDIDISCVKLEQYITGAGEFGEVCSGHLKLPGRKEITVAIKTKSGYT 660
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QY 661 EKORPFLSEASIMQGFDPHNVHLEGVYTKSTPWVITIEFMENGLDSEFLRQNDQGFV 720
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DB 841 QDYRLPPMDCPBALHQLMLDCWQKXRNHRPKFGQIVNTLDKMRNNSLKAMAPLSSGI 900
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RESULT 2
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AC P54763; Q62213; Q9QVY4;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ephrin type-B receptor 2 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor Eph-3) (Neural kinase) (Nuk receptor tyrosine kinase) (SEK-3).
GN EPB2 OR EPH3 OR NUK OR SEK3.
OS Mus musculus (Mouse).
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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94181250; PubMed=8134103;
RA Henkemeyer M., Marengere L.E., McGlade J., Olivier J.P., Conlon R.A., Holmward D.P., Letwin K., Pawson T.,
RT "Immunolocalization of the Nuk receptor tyrosine kinase suggests roles in segmental patterning of the brain and axonogenesis.",
RL Oncogene 9:1001-1014(1994).
RN [2]
RP SEQUENCE OF 516-994 FROM N.A.
RC STRAIN=BALB/C; TISSUE=Brain;
RX MEDLINE=95034306; PubMed=7947319;
RA Becker N., Seltanlou T., Murphy P., Mattei M.-G., Topilko P., Nieto A., Wilkinson D.G., Charnay P., Gialardi P.,
RT "Several receptor tyrosine kinase genes of the Eph family are segmentally expressed in the developing hindbrain.",
RL Mech. Dev. 47:3-17(1994).
RN [3]
RP FUNCTION
RX MEDLINE=20171264; PubMed=10704386;
RA Imondi R., Wideman C., Kaprielian Z.,
RT "Complementary expression of transmembrane ephrins and their receptors in the mouse spinal cord: a possible role in constraining the RT orientation of longitudinally projecting axons.",
RL Development 127:11397-1410(2000).
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RN [4]
RP INTERACTION WITH PRKCAP.
RX MEDLINE=99098206; PubMed=9883737;
RA Torres R., Firestein B.L., Dong H., Staudinger J., Olson E.N., Huganir R.L., Bredt D.S., Gale N.W., Yancopoulos G.D.,
RT "PDZ proteins bind, cluster, and synaptically colocalize with Eph receptors and their ephrin ligands.",
RL Neuron 21:1453-1463(1998).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 29-204.
RX MEDLINE=99066648; PubMed=9853759;
RA Himanen J.-P., Henkemeyer M., Nikolv D.B.,
RT "Crystal structure of the ligand-binding domain of the receptor tyrosine kinase EphB2.",
RL Nature 396:486-491(1998).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 29-208 IN COMPLEX WITH EPHRIN-B2.
RX MEDLINE=21638766; PubMed=11780069;
RA Himanen J.-P., Rajashankar K.R., Lackmann M., Cowan C.A., Henkemeyer M., Nikolv D.B.,
RT "Crystal structure of an Eph receptor-ephrin complex.",
RL Nature 414:933-938(2001).
CC -1- FUNCTION: Receptor for members of the ephrin-B family. Can function in aspects of retinal ganglion cell axon guidance to the optic disk even lacking its tyrosine kinase domain.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
CC -1- SUBUNIT: Interacts with PRKCAP. The ligand-activated form interacts with multiple proteins, including GTPase-activating protein (RASGAP) through its SH2 domain. Binds RASGAP through the juxtamembrane tyrosine residues. Interacts with PRKCAP (by similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in cells of the developing outer retina.
CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin receptor subfamily.
CC -----
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CC -----
DR EMBL, L25890; AAA72411.1; ALT_INIT.
DR EMBL, X76011; CAAS3598.1; -.
DR PDB, 1KGY; 28-MAY-02.
DR PDB, INUK; 13-OCT-99.
DR WGD, WGI; 99611; EphB2.
DR GO; GO:0008046; F:axon guidance receptor activity; IDA.
DR GO; GO:0007411; P:axon guidance; IDA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR001090; Ephrin receptor.
DR InterPro; IPR008957; FN-III-like.
DR InterPro; IPR003961; FN-III.
DR InterPro; IPR003962; FN-III subd.
DR InterPro; IPR008979; Gal_bind-like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001600; SAM.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR InterPro; IPR001426; YKase_receptorV.
DR Pfam; PF01404; EPH_1bd; 1.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00536; SAM; 1.
DR PRINTS; PR0014; FNTYPEIII.
DR PRINTS; PR00109; TYRKINASE.
```

DR Prodom; PD001495; Ephrin receptor; 1.
 DR Prodom; PD000001; Prot kinase; 1.
 DR SMART; SM000615; Eph_1bd; 1.
 DR SMART; SM000600; FN3; 2.
 DR SMART; SM000619; SAM; 1.
 DR SMART; SM000619; TYKc; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN; 1.
 DR PROSITE; PS01107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00101; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS00791; SAM_DOMAIN; 1.
 DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat; 3d-structure.
 FT SIGNAL 1 26
 FT CHAIN 1 26
 FT DOMAIN 27 994
 FT TRANSFEM 27 551
 FT TRANSFEM 552 572
 FT TRANSFEM 573 994
 FT DOMAIN 192 329
 FT DOMAIN 330 439
 FT DOMAIN 440 537
 FT DOMAIN 629 892
 FT DOMAIN 921 985
 FT SITE 992 994
 FT NP_BIND 992 994
 FT BINDING 661 661
 FT ACT_SITE 754 754
 FT MOD_RES 604 604
 FT MOD_RES 610 610
 FT MOD_RES 788 788
 FT MOD_RES 938 938
 FT DISULFID 70 192
 FT DISULFID 105 115
 FT CARBOHYD 273 273
 FT CARBOHYD 344 344
 FT CARBOHYD 436 436
 FT CARBOHYD 490 490
 FT CONFLICT 576 576
 SQ SEQUENCE 994 AA; 110759 MW; BCB9B12A070394C CRC64;
 Query Match 98.9%; Score 5130; DB 1; Length 994;
 Best Local Similarity 99.5%; Pred. No. 2,1e-315;
 Matches 972; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 10 LLLPLLAEEETLMSTTATLGMVHPGSGMEVSGYDENMTIRTYOVCNPFSSQ 69
 DB 18 LLLPLLAEEETLMSTTATLGMVHPGSGMEVSGYDENMTIRTYOVCNPFSSQ 77
 QY 70 NNMRTKFIIRRGARHIVEMKFSVDCSIPSPSCKETFLYYEADPFSATKTFPN 129
 DB 78 NNMRTKFIIRRGARHIVEMKFSVDCSIPSPSCKETFLYYEADPFSATKTFPN 137
 QY 130 WMENPWKVDITIADESFQVDIGRVMKINTFVSFGPVSRSGFYLAFOYDGCMSLIA 189
 DB 138 WMENPWKVDITIADESFQVDIGRVMKINTFVSFGPVSRSGFYLAFOYDGCMSLIA 197
 QY 190 VRYFYRCPRIIONGAIFOETLSGASTSLVARGSCINAEVDPITLYCNCGGEMV 249
 DB 198 VRYFYRCPRIIONGAIFOETLSGASTSLVARGSCINAEVDPITLYCNCGGEMV 257
 QY 250 PIRGCMKAGFEAVENGTVCRGCPSTFRANQDEACTHCPIINSRTTSGAINTVCVRCNGY 309
 DB 258 PIRGCMKAGFEAVENGTVCRGCPSTFRANQDEACTHCPIINSRTTSGAINTVCVRCNGY 317
 QY 310 YRADLDELPMCTTISAPAVISSVNETSLMEPPDPSGGERLVNIIICKSGSGSR 369
 DB 318 YRADLDELPMCTTISAPAVISSVNETSLMEPPDPSGGERLVNIIICKSGSGSR 377
 QY 370 GACTRCGDNVQVAPROGLTEPRITYSDLLAHTQYTFEIOAVNGVTDQSPFSPASVNI 429
 DB 378 GACTRCGDNVQVAPROGLTEPRITYSDLLAHTQYTFEIOAVNGVTDQSPFSPASVNI 437

QY 430 TTNQAPSAVSIKHOVERTVDSITLWSQDPQPGVILDELQYKEKESEYNATAIKSP 489
 DB 438 TTNQAPSAVSIKHOVERTVDSITLWSQDPQPGVILDELQYKEKESEYNATAIKSP 497
 QY 490 TNYTVQGLKAGAIYVQVRAIVYAGIRYSGKNYFOTMTBAEYQISIOEKLPIIIGSSA 549
 DB 498 TNYTVQGLKAGAIYVQVRAIVYAGIRYSGKNYFOTMTBAEYQISIOEKLPIIIGSSA 557
 QY 550 AGVFLAVVYIAVNCRRRGERADSEYTDLOHTYSGHMTPGKIIYIDPFYEDPNEAV 609
 DB 558 AGVFLAVVYIAVNCRRRGERADSEYTDLOHTYSGHMTPGKIIYIDPFYEDPNEAV 617
 QY 610 REFAKEIDISCVKIEQYIAGGEFGEVCSGHIKLPKKEIFVAIKTLKGYTEKQRDFLS 669
 DB 618 REFAKEIDISCVKIEQYIAGGEFGEVCSGHIKLPKKEIFVAIKTLKGYTEKQRDFLS 677
 QY 670 EASIMGQDHPNVHLHGVVTKSTPVMILTEFENGLSDSFLRNDQGFVIOVGLWLRG 729
 DB 678 EASIMGQDHPNVHLHGVVTKSTPVMILTEFENGLSDSFLRNDQGFVIOVGLWLRG 737
 QY 730 IAAGKYLADKNVYHRDLAARNILVNSNLVCKYDFGLSRFLBEDTSDPTYSALGKIP 789
 DB 738 IAAGKYLADKNVYHRDLAARNILVNSNLVCKYDFGLSRFLBEDTSDPTYSALGKIP 797
 QY 790 IRTWAPENIYRKRTSDVWSYGIWVWEVNSYGERPYMTNODVYNALIEQYRLPPM 849
 DB 798 IRTWAPENIYRKRTSDVWSYGIWVWEVNSYGERPYMTNODVYNALIEQYRLPPM 857
 QY 850 DCPBALHQLMDCQXKRNHRPKFGQIVNTLDKXIRPNLSLKMAPLSSGINPLDRTI 909
 DB 858 DCPBALHQLMDCQXKRNHRPKFGQIVNTLDKXIRPNLSLKMAPLSSGINPLDRTI 917
 QY 910 PDYTSFNTDWEALIKGQYKESFANAFTSPVVSQMMEDILRGVTLAHOXKILN 969
 DB 918 PDYTSFNTDWEALIKGQYKESFANAFTSPVVSQMMEDILRGVTLAHOXKILN 977
 QY 970 SIQVRAQMNQIOSVEV 986
 DB 978 SIQVRAQMNQIOSVEV 994

RESULT 3
 EPH2 CHICK
 ID EPH2 CHICK STANDARD; PRT; 1004 AA.
 AC P28653;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ephrin type-B receptor 2 precursor (EC 2.7.1.112) (Tyrosine-protein
 DE kinase receptor CEK5).
 GN EPHB2 OR CEK5.
 OS Gallus gallus (chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).
 RC Tissue=Embryo;
 RX MEDLINE=9214672; PubMed=1664238;
 RA Pasquale E.B.;
 RT "Identification of chicken embryo tyrosine kinase 5, a developmentally
 RT regulated receptor-type tyrosine kinase of the Eph family";
 RL Cell Regul. 2:523-534(1991).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
 RC Tissue=Brain;
 RX MEDLINE=93286394; PubMed=8510926;
 RA Sajjadi F.G.; Pasquale E.B.;
 RT "Five novel avian Eph-related tyrosine kinases are differentially
 RT expressed";
 RL Oncogene 8:1807-1813(1993).

CC - FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. PROBABLY AN
CC IMPORTANT COMPONENT OF SIGNAL TRANSDUCTION PATHWAYS.
CC - CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC - SUBCELLULAR LOCATION: Type I membrane protein.
CC - ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2:
CC Name=long; Synonyms=CEK5+; Sequence=displayed;
CC Name=short;
CC IsoId=P28693-1; Sequence=displayed;
CC IsoId=P28693-2; Sequence=VSP_003018;
CC - TISSUE SPECIFICITY: WIDE TISSUE DISTRIBUTION THROUGHOUT
CC DEVELOPMENT AND SUSTAINED EXPRESSION IN ADULT BRAIN. THE LONGER
CC FORM (CEK5+) IS SPECIFICALLY EXPRESSED IN THE CENTRAL NERVOUS
CC SYSTEM.
CC - SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
CC - SIMILARITY: Contains 2 fibronectin type III domains.
CC - SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin
CC receptor subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, M63325; AAA48667.1; ALT_INIT.
DR PDB, 1S9G; 06-OCT-99.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR001090; Ephrin_receptor.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008978; Gal_bind_like.
DR InterPro: IPR007719; POC_kinase.
DR InterPro: IPR001245; SAM.
DR InterPro: IPR008266; Tyr_kinase_AS.
DR InterPro: IPR001426; YKase_receptor_V.
DR Pfam: PF01404; Eph_Ibd_1.
DR Pfam: PF00041; fn3_2.
DR Pfam: PF00069; PKinase_1.
DR Pfam: PF00536; SAM_1.
DR PRINTS; PR00014; ENTPEIIT.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD001495; Ephrin_receptor; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00615; EPH_Ibd_1.
DR SMART; SM00060; FN3_2.
DR SMART; SM00454; SAM; 1.
DR SMART; SM00219; TYKc; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS50791; RECEPTOR_TYR_KIN_V_2; 1.
DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KM Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing;
KM Repeat; 3d-structure; 19
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 1004 EPHRIN TYPE-B RECEPTOR 2.
FT DOMAIN 20 544 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 545 565 POTENTIAL.
FT DOMAIN 566 1004 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 20 321 CYS-RICH.
FT DOMAIN 326 419 FIBRONECTIN TYPE-III 1.
FT DOMAIN 437 521 FIBRONECTIN TYPE-III 2.
FT DOMAIN 639 902 PROTEIN KINASE.
FT DOMAIN 931 995 SAM.

FT SITE 1002 1004 PDZ-BINDING MOTIF (POTENTIAL).
FT NP_BIND 645 653 ATP (BY SIMILARITY).
FT BINDING 671 671 ATP (BY SIMILARITY).
FT ACT_SITE 764 764 BY SIMILARITY.
FT MOD_RES 614 614 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 620 620 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 798 798 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 948 948 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 429 429 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 478 478 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARPELIC 591 606 Missing (in isoform short).
FT /FtId=Vsp_003018
SQ SEQUENCE 1004 AA; 11963 MW; 8D2621970EC6E0 CRC64;
Query Match 95.9%; Score 4975.5; DB 1; Length 1004;
Best Local Similarity 94.3%; Pred. No. 1.2e-305;
Matches 937; Conservative 28; Mismatches 12; Indels 17; Gaps 2;
10 LLLPLAAVEETLMDSTTATLAEIGMWHPPSGHEVSGYDENNTTITTYQVNCVFESSQ 69
11 LALPLAAVEETLMDSTTATLAEIGMWHPPSGHEVSGYDENNTTITTYQVNCVFESSQ 70
70 NNMILTKFIRRGARHIVENKFSVDCSSIPSPGSCKETFNLYYEADPDSATKTPFPN 129
71 NNMILTKFIRRGARHIVENKFSVDCSSIPSPGSCKETFNLYYEADPDSATKTPFPN 130
130 WMENFWKVDITIAADESPQVDLGRVWKINTEVRSFPGVSRSGFYLAFOYGGMSLIA 189
131 WMENFWKVDITIAADESPQVDLGRVWKINTEVRSFPGVSRSGFYLAFOYGGMSLIA 190
190 VVVFYKCPRIIONGAIPOETLSGAEISTLVAAGSCITANAEVDVPIKLYCNGGEMTLV 249
191 VVVFYKCPRIIONGAIPOETLSGAEISTLVAAGSCITANAEVDVPIKLYCNGGEMTLV 250
250 PIGRCMCAGEAVENGTVGRCGSPGTFKANQSGEACTHCINSRTTSEGANVCYCRNGY 309
251 PIGRCMCAGEAVENGTVGRCGSPGTFKANQSGEACTHCINSRTTSEGANVCYCRNGY 310
310 YRADLCPDMCCTTPSPQAVISSVNETSLMETPTPDSGSGEDLYNNIICKSCSGR 369
311 YRADLCPDMCCTTPSPQAVISSVNETSLMETPTPDSGSGEDLYNNIICKSCSGR 370
370 GACTRCGDNVQYARQGLTEPRYISDLAHTQYTEEIQAVNGVTQSPSPQFASVNI 429
371 GACTRCGDNVQYARQGLTEPRYISDLAHTQYTEEIQAVNGVTQSPSPQFASVNI 430
430 TTNQAPPAVAVSIMQVSTVDSITLSMSQPDQNGVILIDELYEKELSNNTATASP 489
431 TTNQAPPAVAVSIMQVSTVDSITLSMSQPDQNGVILIDELYEKELSNNTATASP 490
490 TTNVVOGLKAGATVFCVARTVAGYGRYSGKMYFCMTAEVQTSIOECLPIIGSSA 549
491 TTNVVOGLKAGATVFCVARTVAGYGRYSGKMYFCMTAEVQTSIOECLPIIGSSA 550
550 AGVFLAVAVVIAVCNRRGFESADSEYDKLCHYTSGR-----MTFG 592
551 AGVFLAVAVVIAVCNRRGFESADSEYDKLCHYTSGR-----MTFG 593
593 MKIYIDPFTYEDPDEAVAEFAKEIDISCVKLEQVYIGAGEFEVSGSHKLPGRKEIFPAI 652
611 MKIYIDPFTYEDPDEAVAEFAKEIDISCVKLEQVYIGAGEFEVSGSHKLPGRKEIFPAI 670
653 KTKSGYTEKORPDLSPASIMQFDHENVILHGGVYTKSPVMIITEFMENGSLDSFLR 712
671 KTKSGYTEKORPDLSPASIMQFDHENVILHGGVYTKSPVMIITEFMENGSLDSFLR 730
713 QNDGQFTYICVGMIRGIAAGMYLADNMYVHRRLAARNILVSNLVCVKSDFLSRFL 772
731 QNDGQFTYICVGMIRGIAAGMYLADNMYVHRRLAARNILVSNLVCVKSDFLSRFL 790

QY 773 DDTSDPTVYALGKIPDIRNTAPEAIQYRFTSASDWSYGIYMEVMSYGERPYDMMN 832
 Db 791 DDTSDPTVYALGKIPDIRNTAPEAIQYRFTSASDWSYGIYMEVMSYGERPYDMMN 850
 QY 833 QDVNMA.EQDYRL.PPMDPCSAALHQLM.LDCMKDRNRH.PFGQIVNTLDMKINPNSLXA 892
 Db 851 QDVNMA.EQDYRL.PPMDPCSAALHQLM.LDCMKDRNRH.PFGQIVNTLDMKINPNSLXA 910
 QY 893 MAPSSGIN.PLDRITPDYTSFNTVDEMLAIRMGOYKESFANAGFTSDVTSQMMED 952
 Db 911 MAPSSGIN.PLDRITPDYTSFNTVDEMLAIRMGOYKESFANAGFTSDVTSQMMED 970
 QY 953 ILRLGVTLAHHOKKILNSIQVRAQNNQIQSVEV 986
 Db 971 ILRLGVTLAHHOKKILNSIQVRAQNNQIQSVEV 1004

RESULT 4
 EPH2_COTUA STANDARD; PRT; 987 AA.
 ID ID EPH2_COTUA STANDARD; PRT; 987 AA.
 AC 090344;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ephrin type-B receptor 2 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor QKES).
 GN EPH2 OR QKES.
 OS Coturnix coturnix japonica (Japanese quail).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Coturnix.
 OC NCBI_TaxID=93934;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=9610331; PubMed=8612986;
 RA Kenny D., Bromner-Frazer M., Marcelle C.;
 RT "The receptor tyrosine kinase QKES mRNA is expressed in a gradient within the neural retina and the tectum."
 RL Dev. Biol. 172:708-716(1995).
 CC -1- FUNCTION: Receptor for members of the ephrin-B family.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin receptor subfamily.
 CC -----
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 CC -----
 DR EMBL; X91737; CAAG2862.1; .
 DR HSSP; P29323; 1B4F.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR001090; Ephrin_receptor.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR003962; FNIII_subd.
 DR InterPro; IPR008978; Gal_bind_like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001660; SAM.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008265; Tyr_kinase_AS.
 DR InterPro; IPR001426; Ykase_receptorV.
 DR Pfam; PF01404; EPH_1bd. 1.
 DR Pfam; PF00041; fn3_2.
 DR Pfam; PF00069; Pkinase; 1.

DR Pfam; PF00536; SAM; 1.
 DR PRINTS; PS00014; FNYPEI1.
 DR PRINTS; PS00109; TYRKINASE.
 DR ProDom; PD001495; Ephrin_receptor; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00615; EPH_1bd. 1.
 DR SMART; SM00060; FN3_2.
 DR SMART; SM00454; SAM; 1.
 DR SMART; SM00219; TYKC; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; FALSE_NEG.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS50105; SAM_DOMAIN; 1.
 DR TRANSFERASE; Tyrosine-protein kinase; ATP-binding; Phosphorylation; Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 KW SIGNAL
 FT SIGNAL 1 19
 FT CHAIN 20 987
 FT DOMAIN 20 544
 FT TRANSMEM 545 565
 FT DOMAIN 566 987
 FT DOMAIN 185 432
 FT DOMAIN 323 530
 FT DOMAIN 433 530
 FT DOMAIN 622 885
 FT DOMAIN 914 978
 FT SITE 985 987
 FT NP_BIND 628 636
 FT BINDING 654 654
 FT ACT_SITE 747 747
 FT MOD_RES 597 597
 FT MOD_RES 603 603
 FT MOD_RES 781 781
 FT MOD_RES 931 931
 FT CARBOHYD 266 266
 FT CARBOHYD 337 337
 FT CARBOHYD 429 429
 FT CARBOHYD 478 478
 FT CARBOHYD 483 483
 SQ SEQUENCE 987 AA; 110331 MW; 05DECC68B718D07 CRC64;
 Query Match 95.3%; Score 4945; DB 1; Length 987;
 Best Local Similarity 94.9%; Pred. No. 9.5e-304;
 Matches 927; Conservative 30; Mismatches 20; Indels 0; Gaps 0;
 QY 10 LLLPLAAVEETLMDSTTATAEIGMWHPPSGWEVSYGVDENNITRTYQVCNVPESQ 69
 Db 11 LALLPLAAVEETLMDSTTATAEIGMWHPPSGWEVSYGVDENNITRTYQVCNVPESQ 70
 QY 70 NNMULTFIRRGARHIVHEKESVRCSSIPVPSCKETFNLYYEADPDSATKTFN 129
 Db 71 NNMULTFIRRGARHIVHEKESVRCSSIPVPSCKETFNLYYEADPDSATKTFN 130
 QY 130 WNEPWWVVDITIADESFSQVDLGRVYKINTVRSFGPVSRSGFYLAPODYGCMSLIA 189
 Db 131 WNEPWWVVDITIADESFSQVDLGRVYKINTVRSFGPVSRSGFYLAPODYGCMSLIA 190
 QY 190 VRFVYRKCPRIIINGAIFQETLSAESTSLVAVRGSCIANAEVDVPIKYCNGDGWLV 249
 Db 191 VRFVYRKCPRIIINGAIFQETLSAESTSLVAVRGSCIANAEVDVPIKYCNGDGWLV 250
 QY 250 PIGSCWCAKGEAENGTVCGSPGSGFTFKANQGEACTHCPINSRTSSEGAATNCVNGY 309
 Db 251 PIGSCWCAKGEAENGTVCGSPGSGFTFKANQGEACTHCPINSRTSSEGAATNCVNGY 310
 QY 310 YRADLDPLDMECTTIPAPQAVISSVNETSLIMLWTPPRDSGGREDIVNIICKSCSGR 369
 Db 311 YRADLDPLDMECTTIPAPQAVISSVNETSLIMLWTPPRDSGGREDIVNIICKSCSGR 370
 QY 370 GACTRCGNNVQYARQIGTEPRRIYISDLAHTQYTEIGAVNGVTDQSPFSPAFASVI 429


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Db 371 GACTRCGDNVQFAPRQGLTEPRRIYISDLLAHTQYTFEIQAVNGVTDQSPFSPQFASVNI 430
QY 430 TTNOAPSASIMHOVSRTVDSITLWSOPDQPNVILDELOYEKELESEVATAIKSP 489
Db 431 TTNOAPSASIMHOVSRTVDSITLWSOPDQPNVILDELOYEKELESEVATAIKSP 490
QY 490 TMTVTVOGLKAGAIYFVOVARTVAGYGRYSGMYFQMTAEYQTSIQEKLPLIIGSSA 549
Db 491 TMTVTVOGLKAGAIYFVOVARTVAGYGRYSGMYFQMTAEYQTSIQEKLPLIIGSSA 550
QY 550 AGIVFLIAVVVILVCRRRGPFRADSEYTDKLOHTSGHNTPGMKIYIDPFTYEDPNEAV 609
Db 551 AGIVFLIAVVVILVCRRRGPFRADSEYTDKLOHTSGHNTPGMKIYIDPFTYEDPNEAV 610
QY 610 REFAKEIDISCVKIEQYIGAGEFGEVCSGHLKLPKKEIFVAIKTLKSGYTEKORRDFLS 669
Db 611 REFAKEIDISCVKIEQYIGAGEFGEVCSGHLKLPKKEIFVAIKTLKSGYTEKORRDFLS 670
QY 670 BASIMGQFDPHNVYHLEGVYTKSTPVWITTEFMENGLSDSFLRQNDQGFVTIQLVGMIRG 729
Db 671 BASIMGQFDPHNVYHLEGVYTKSTPVWITTEFMENGLSDSFLRQNDQGFVTIQLVGMIRG 730
QY 730 IAAGMXYLADNMYVHRDLARNTLVNSNLVCKVSDFLSRFLEDDTSDPTYSALGGKIP 789
Db 731 IAAGMXYLADNMYVHRDLARNTLVNSNLVCKVSDFLSRFLEDDTSDPTYSALGGKIP 790
QY 790 IRMTAPEAIQYRKFTSADVMSYGIWMEVMSYGERPYWDMTNQDVINAIEQDYRLPPM 849
Db 791 IRMTAPEAIQYRKFTSADVMSYGIWMEVMSYGERPYWDMTNQDVINAIEQDYRLPPM 850
QY 850 DCPSAHQMLDQWQXDRNHRPKFGQIVNTLDKMINPNSLKAMAPLSSGINPLDRTI 909
Db 851 DCPSAHQMLDQWQXDRNHRPKFGQIVNTLDKMINPNSLKAMAPLSSGINPLDRTI 910
QY 910 PDYTSFNTVDEMLEAIKMGQYKESFANAGFTSFDVYSOMMEDILRLGVTLAGHCKKILN 969
Db 911 PDYTSFNTVDEMLEAIKMGQYKESFANAGFTSFDVYSOMMEDILRLGVTLAGHCKKILN 970
QY 970 SIQVMAQNNQIOSVEY 986
Db 971 SIQVMAQNNQIOSVEY 987

```

Search completed: August 28, 2004, 04:09:26
 Job time : 20.3577 secs

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Gencore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2004, 04:02:25 ; Search time 31.8844 Seconds
(without alignments)
2974.650 Million cell updates/sec

Title: US-09-914-883-2
Perfect score: 5188
Sequence: 1 MALRRGALLLLPLLAIVE.....IINSIQVRAQNMQIQSVEV 986

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 segs, 96191526 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 90%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:***
1: p1r1:***
2: p1r2:***
3: p1r3:***
4: p1r4:***

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5089	98.1	970	2	178842 receptor protein-t
2	4993.5	96.3	995	2	A56599 embryo kinase 5 -

ALIGNMENTS

RESULT 1
178842
receptor protein-tyrosine kinase - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 29-May-1998 #sequence_revision 29-May-1998 #ext_change 16-Jun-1999
C/Accession: 178842
R/Box, G.M.; Holley, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu, R.; Welch,
Oncogene 10, 897-905, 1995
A/Title: cDNA cloning and tissue distribution of five human EPH-like receptor protein-ty
A/Reference number: 158351; MUID:95206782; PMID:7898931
A/Accession: 178842
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-970 <RES>
A/Cross-references: GB:U36643; NID:9551609; PIDN:AAA74244.1; PID:9551610
C/Genetics:
A/Gene: HEK5
C/Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
F:603-871/Domain: protein kinase homology <KIN>
F:894-960/Domain: SAM homology <SAM>

Query Match 98.1%; Score 5089; DB 2; Length 970;

Best Local Similarity 99.4%; Pred. No. 5.3e-231;
Matches 966; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY	15	LLAAVEETLMDSTATAELGMVHPPSGMEVSGYDENMNTIRTYQVGNVFESSQNMWR	74
DB	1	LLAAVEETLMDSTATAELGMVHPPSGMEVSGYDENMNTIRTYQVGNVFESSQNMWR	60
QY	75	TKFIRRGARHRYHEMKSVYRDCSSIPSPGCKETENLYYYEADFPSATCTFPMWENP	134
DB	61	TKFIRRGARHRYHEMKSVYRDCSSIPSPGCKETENLYYYEADFPSATCTFPMWENP	120
QY	135	WYKVDITIADESFSQVDIGRWKINTEVRSFGVSRSGFYLAQDYGGCNSLIAVRYFY	194
DB	121	WYKVDITIADESFSQVDIGRWKINTEVRSFGVSRSGFYLAQDYGGCNSLIAVRYFY	180
QY	195	RKCPRIIONGAIPOETLSGASTSLVARGSCINAEEDVPILKYCNGDEMIYPIGRG	254
DB	181	RKCPRIIONGAIPOETLSGASTSLVARGSCINAEEDVPILKYCNGDEMIYPIGRG	240
QY	255	MCKAGFEAVENGTVRCGCPGCTFKANQGDCACTHCPIINSRTSAGATNCVCRNGYRADL	314
DB	241	MCKAGFEAVENGTVRCGCPGCTFKANQGDCACTHCPIINSRTSAGATNCVCRNGYRADL	300
QY	315	DPLDMPCTTISAPQAVYSSVNETSLMLEWTPPRDSGREDLVNIIKSCGSGRGACTR	374
DB	301	DPLDMPCTTISAPQAVYSSVNETSLMLEWTPPRDSGREDLVNIIKSCGSGRGACTR	360
QY	375	CGDNQVAPROGLTEPRYISDLAHTQYTFEIOAVNGVTDQSPFSPQFASVNTTNOA	434
DB	361	CGDNQVAPROGLTEPRYISDLAHTQYTFEIOAVNGVTDQSPFSPQFASVNTTNOA	420
QY	435	APSASVIMHGVSRIVDSITLISWSQPDQNGVILDEYLOVYKEUSEYNALIKSPTNTVT	494
DB	421	APSASVIMHGVSRIVDSITLISWSQPDQNGVILDEYLOVYKEUSEYNALIKSPTNTVT	480
QY	495	VQGLKAGAIYVQVAVRIVAGYRGSKMYPQMTAEAYQYSIOEKPLITIGSSAAGLVF	554
DB	481	-GLKAGAIYVQVAVRIVAGYRGSKMYPQMTAEAYQYSIOEKPLITIGSSAAGLVF	538
QY	555	LIAVVVIAIVCNRRGFERADSEYTDKLOHTSGHMTPMKTIYIDPFYEDPNEAVREPAK	614
DB	539	LIAVVVIAIVCNRRGFERADSEYTDKLOHTSGHMTPMKTIYIDPFYEDPNEAVREPAK	598
QY	615	EIDISCYVLEIQTGGEFVCSGHLKPKRREIFVAIKTILKSGYTERQORDPLSEASIM	674
DB	599	EIDISCYVLEIQTGGEFVCSGHLKPKRREIFVAIKTILKSGYTERQORDPLSEASIM	658
QY	675	GOFDHPNTYHLEGVYTKSTPVMIIITEFMENGLSDSFLEQNDGQFTVIOVGLMGLIAAGM	734
DB	659	GOFDHPNTYHLEGVYTKSTPVMIIITEFMENGLSDSFLEQNDGQFTVIOVGLMGLIAAGM	718
QY	735	KYLADMTYVHRDLAARNILVNSNLVCKVSDGLSFLFEDDTSDDPYTVALGKRPIMRTA	794
DB	719	KYLADMTYVHRDLAARNILVNSNLVCKVSDGLSFLFEDDTSDDPYTVALGKRPIMRTA	778
QY	795	PBAIQPKFTASDVMSYGIYVWEVMSYGERPYMDNTQDYNALIEQYRPLPPEDCCSA	854
DB	779	PBAIQPKFTASDVMSYGIYVWEVMSYGERPYMDNTQDYNALIEQYRPLPPEDCCSA	838
QY	855	LHQLMDCQKDRNRPRFGQIVNTLDKIRNPNSLKMAAPLSSGINSPLDRTIPDYTS	914
DB	839	LHQLMDCQKDRNRPRFGQIVNTLDKIRNPNSLKMAAPLSSGINSPLDRTIPDYTS	898
QY	915	FNTVDEWEIATMGQYKESFANAGTSPDVVSOMMMEDILKGLVLAHQKILINSIQVM	974
DB	899	FNTVDEWEIATMGQYKESFANAGTSPDVVSOMMMEDILKGLVLAHQKILINSIQVM	958
QY	975	RAQNMQIQSVEV 986	
DB	959	RAQNMQIQSVEV 970	

RESULT 2

A56599
 embryo kinase 5 - chicken
 N:Alternate names: receptor tyrosine kinase Ceks
 N:Contains: protein-tyrosine kinase (EC 2.7.1.112)
 C:Species: Gallus gallus (chicken)
 C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 04-Feb-2000
 C:Accession: A56599
 R:Paquale, E.B.
 Cell Regul. 2, 523-534, 1991
 A:Title: Identification of chicken embryo kinase 5, a developmentally regulated receptor
 A:Reference number: A56599; MUID:92144672; PMID:1664238
 A:Accession: A56599
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-995 <PMS>
 A:Cross-references: GB:M62325; NID:g211448; PIDN:AAA48667.1; PID:g211449
 A>Note: sequence extracted from NCBI backbone (NCBI:81939; NCBI:P:62001)
 C:Superfamily: protein-tyrosine kinase, receptor type eph, fibronectin type III repeat
 C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein ki
 F:628-896/Domain: protein kinase homology <KIN>
 F:636-644/Region: protein kinase ATP-binding motif
 F:919-985/Domain: SAM homology <SAM>

Query Match 96.3%; Score 4993.5; DB 2; Length 995;
 Best Local Similarity 95.8%; Pred. No. 1.6e-226;
 Matches 937; Conservative 28; Mismatches 12; Indels 1; Gaps 1;

QY 10 LLLPLAAVETLMDSTTAELGMYVHPSCGMEVSYGDEMNTIRTYQVQNVFSSQ 69
 DB 18 LALLPLAAVETLMDSTTAELGMYVHPSCGMEVSYGDEMNTIRTYQVQNVFSSQ 77
 QY 70 NNMRLTKFIRRRGAHRIHVEKFSVRDSSIPSVPGSCKETFNLYYEADFDSATKTFPN 129
 DB 78 NNMRLTKFIRRRGAHRIHVEKFSVRDSSIPSVPGSCKETFNLYYEADFDSATKTFPN 137
 QY 130 WMENPMKVVDTIADDSFSQVDLGRVWKINTEVRSFGVSRSGFYLAFODYGCMSLIA 189
 DB 138 WMENPMKVVDTIADDSFSQVDLGRVWKINTEVRSFGVSRSGFYLAFODYGCMSLIA 197
 QY 190 VRVFRKCPRIIONGAIFOETLSGAEISTLVAARGSCIANAEEDVPIKLYCNGDEWLY 249
 DB 198 VRVFRKCPRIIONGAIFOETLSGAEISTLVAARGSCIANAEEDVPIKLYCNGDEWLY 257
 QY 250 PIGRCMKAGFEAVENGTVCRGCPSTFKANQGDCACTHCPINSRTTSGATNCVCRNGY 309
 DB 258 PIGRCMKAGFEAVENGTVCRGCPSTFKANQGDCACTHCPINSRTTSGATNCVCRNGY 317
 QY 310 YRDLPLDMPCTTIPAPQAVISSVNETSLMLETPPRDGGREDLVYNIICKSGSGR 369
 DB 318 YRDLPLDMPCTTIPAPQAVISSVNETSLMLETPPRDGGREDLVYNIICKSGSGR 377
 QY 370 GACTRCGDNVQYAPRQGLTEPRYISDLAHTQYFEIQAVNGVTDQSPFPASVNI 429
 DB 378 GACTRCGDNVQYAPRQGLTEPRYISDLAHTQYFEIQAVNGVTDQSPFPASVNI 437
 QY 430 TTNQAPSAVSIMQVSRVDSITLSWQDPQNGVILDYELQYKEKSEVNATAIKSP 489
 DB 438 TTNQAPSAVSIMQVSRVDSITLSWQDPQNGVILDYELQYKEKSEVNATAIKSP 497
 QY 490 TNYTVQGLKAGAIYVQVBARIVAGYGRYSGKVFQMTAEYQTSIQEKLPLIIGSSA 549
 DB 498 TNYTVQGLKAGAIYVQVBARIVAGYGRYSGKVFQMTAEYQTSIQEKLPLIIGSSA 557
 QY 550 AGLVFLAAVVVIAVGN-REGFERADSEYTDKLOHTSGHMPGKTIYIDPFTYEDPNEA 608
 DB 558 AGLVFLAAVVVIAVGN-REGFERADSEYTDKLOHTSGHMPGKTIYIDPFTYEDPNEA 617
 QY 609 VRFAKEIDISCVKIEOVIGAGEFVSGHKLPGKREIFVAIKTLKSGYTEKQRDFL 668
 DB 618 VRFAKEIDISCVKIEOVIGAGEFVSGHKLPGKREIFVAIKTLKSGYTEKQRDFL 677
 QY 669 SEASIMQGFHPNVITHLEGVYTKSTPVMITTEMNGSLDSFLKQNDGQFTVQLVGMNR 728

DB 678 SEASIMQGFHPNVITHLEGVYTKSTPVMITTEMNGSLDSFLKQNDGQFTVQLVGMNR 737
 QY 729 GIAAGKTLADNNVYHRDLAARNILVNSNLVCXVSDFGLSRFLBEDTSDPTYSALGGKI 788
 DB 728 GIAAGKTLADNNVYHRDLAARNILVNSNLVCXVSDFGLSRFLBEDTSDPTYSALGGKI 797
 QY 789 PIRMTAPPAIOYRKETSASDVMSYGIYVMEVMSYGERPYMTNODVINAIEODYRPLPP 848
 DB 798 PIRMTAPPAIOYRKETSASDVMSYGIYVMEVMSYGERPYMTNODVINAIEODYRPLPP 857
 QY 849 MDPSALHQLMDQWQXDRNHRPKFGQIVNTLDKXIRNPNSLKAMAPLSSGINTPLDRT 908
 DB 858 MDPSALHQLMDQWQXDRNHRPKFGQIVNTLDKXIRNPNSLKAMAPLSSGINTPLDRT 917
 QY 909 IPDYTSNTVDENLEAITMGQYKESFANAQSTSDVYSQMMEDILRLGVTLAQHKKIL 968
 DB 918 IPDYTSNTVDENLEAITMGQYKESFANAQSTSDVYSQMMEDILRLGVTLAQHKKIL 977
 QY 969 NSIQVMRAQNMQIOSVEY 986
 DB 978 NSIQVMRAQNMQIOSVEY 995

Search completed: August 28, 2004, 04:14:04
 Job time: 31.8844 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2004, 04:00:54 ; Search time 97.1024 Seconds

(without alignments)
3203.844 Million cell updates/sec

Title: US-09-914-883-2

Perfect score: 5188

Sequence: 1 MALRLGALLLPLLAIVE.....LINSIQVFAQNNQIQSVFV 986

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 90%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_archaea:*
2: SP_bacteria:*
3: SP_fungi:*
4: SP_human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP Vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriap:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5130	98.9	994	11	Q9GVY4 Q9GVY4 mus sp. neu

ALIGNMENTS

RESULT 1
Q9GVY4 PRELIMINARY; PRT; 994 AA.
AC Q9GVY4; 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Neutral kinase, NUK=EPH/ELK/ECK family receptor-like tyrosine kinase (EC 2.7.1.112) (Ephrin receptor) (Tyrosine-protein kinase receptor).
DE receptor).

OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94181250; PubMed=8134103;
RA Henkemeyer M., Marengue U.E., Mogliade J., Olivier J.P., Conlon R.A.,
RA Holmuyard D.P., Letwin K., Pawson T.,
RT "Immunolocalization of the Nuk receptor tyrosine kinase suggests roles
RT in segmental patterning of the brain and axonogenesis.",
RL Oncogene 9:1001-1014(1994).
CC -1 CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
CC TYROSINE PHOSPHATE
CC -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY)
CC -1 SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
CC RECEPTOR SUBFAMILY.
DR HSSP; P29323; 184F.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005003; F:ephrin receptor activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR InterPro; IPR006309; EGF-like.
DR InterPro; IPR001890; Ephrin_receptor.
DR InterPro; IPR003962; FNIII_subd.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008857; FN_III-like.
DR InterPro; IPR008879; Gal_bind-like.
DR InterPro; IPR000719; Prol_kinase.
DR InterPro; IPR001660; SAM.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR InterPro; IPR001426; Ykase_receptorov.
DR Pfam; PF01404; EPH_lbd; 1.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00069; kinase; 1.
DR Pfam; PF00536; SAM; 1.
DR PRINTS; PR00014; ENTYPETII.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD001495; Ephrin_receptor; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00615; EPH_lbd; 1.
DR SMART; SM00060; FN3_2.
DR SMART; SM00454; SAM; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PS50105; SAM_DOMAIN; 1.
KW ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor; Repeat;
KW Transferrase; Transmembrane; Tyrosine-protein kinase.
SQ SEQUENCE 994 AA; 110759 MW; BC6B9B12A070394C CRC64;

Query Match 98.9%; Score 5130; DB 11; Length 994;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 972; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 10 LLLPLLAVERETLNDSTTATATGMMVHPSPGMEVSGYDENMNTIRTYQVGVFESSQ 69
DB 18 LLLPLLAVERETLNDSTTATATGMMVHPSPGMEVSGYDENMNTIRTYQVGVFESSQ 77
QY 70 NNMWLATKTRRGGARIRHVEKFSVRCDSSTPSVPGSKETFFNLYYVADSDATKTFPN 129
DB 78 NNMWLATKTRRGGARIRHVEKFSVRCDSSTPSVPGSKETFFNLYYVADSDATKTFPN 137
QY 130 WMENPMVAVDIIADEFSGVDLGGRVKVKINTEVRSFGPVSRSGFYLAFDYGGCMSLIA 189

Db	138	WMENPWYKVDITIAADESFSQVLDLGRYMKINTEVRSRGPYSRNGFYIAFODYGGCKSLIA	197
Qy	190	VRVYFKCPRIIONGAIFOETLSGABSTLVAARGSCIANAEVDPKLYCNGDEMLV	249
Db	198	VRVYFKCPRIIONGAIFOETLSGABSTLVAARGSCIANAEVDPKLYCNGDEMLV	257
Qy	250	PIGCMCKAGFEAVENGTVCRCGSPGFKANOGDEACTHCPINSRTTSEGATNCVCRNGY	309
Db	258	PIGCMCKAGFEAVENGTVCRCGSPGFKANOGDEACTHCPINSRTTSEGATNCVCRNGY	317
Qy	310	YRADLDPLDMPCTTTPAPQAVISVNETSLMLEWTPPRDSCGREDLVNIIICKSCGSR	369
Db	318	YRADLDPLDMPCTTTPAPQAVISVNETSLMLEWTPPRDSCGREDLVNIIICKSCGSR	377
Qy	370	GACTRCGDNYQVAPROGLTEPRITYSDLAHTQYFETIOAVNGVTDQSPSPQFASVNI	429
Db	378	GACTRCGDNYQVAPROGLTEPRITYSDLAHTQYFETIOAVNGVTDQSPSPQFASVNI	437
Qy	430	TTNOAPSASVIMHOVSRTVDSITLSWSQDPQNGVILDYELQYKEKELSEYNATAIKSP	489
Db	438	TTNOAPSASVIMHOVSRTVDSITLSWSQDPQNGVILDYELQYKEKELSEYNATAIKSP	497
Qy	490	TNTVTVOGLKAGAIYVQVAPRTVAGYGRYSKMYFQMTFAYQTSIQEKLPIIIGSSA	549
Db	498	TNTVTVOGLKAGAIYVQVAPRTVAGYGRYSKMYFQMTFAYQTSIQEKLPIIIGSSA	557
Qy	550	AGLVEFLAVVVAIVCNRSGFERADSEYTDKLOHYTSGHMPGMKIYIDPFTYEDPNEAV	609
Db	558	AGLVEFLAVVVAIVCNRSGFERADSEYTDKLOHYTSGHMPGMKIYIDPFTYEDPNEAV	617
Qy	610	REFAKEIDISCVIEQYIGAGEFGEVCSGHLKPGKREIFVAIKTLKSGYTEKORDFLS	669
Db	618	REFAKEIDISCVIEQYIGAGEFGEVCSGHLKPGKREIFVAIKTLKSGYTEKORDFLS	677
Qy	670	EASIMGQFDPHNYIHLGGVTKSTPYMIITEFMENGLSDSFLRQNDGQFTVIQVGMLRG	729
Db	678	EASIMGQFDPHNYIHLGGVTKSTPYMIITEFMENGLSDSFLRQNDGQFTVIQVGMLRG	737
Qy	730	IAAGMKYLDAMNYVHRDLAARNILVNSNLVCVSDFLSRFLEDDTSDPTYSALGKIP	789
Db	738	IAAGMKYLDAMNYVHRDLAARNILVNSNLVCVSDFLSRFLEDDTSDPTYSALGKIP	797
Qy	790	IRWTAPBAIQYRKFTSASDVWSYGIWMEVMSYGERPYWDMTNQDVYINAIEODYRLPPM	849
Db	798	IRWTAPBAIQYRKFTSASDVWSYGIWMEVMSYGERPYWDMTNQDVYINAIEODYRLPPM	857
Qy	850	DCEPALHQLMLDCWQKDRNHRPKFQIVNTLDMIRNPNLSKAMAPLSSGINLPLDRTI	909
Db	858	DCEPALHQLMLDCWQKDRNHRPKFQIVNTLDMIRNPNLSKAMAPLSSGINLPLDRTI	917
Qy	910	PDYTSNTYVDEMELEAIKMGQYKESFANAGFTSPDVVSQMMEDILRLGYTLAGHOKKILN	969
Db	918	PDYTSNTYVDEMELEAIKMGQYKESFANAGFTSPDVVSQMMEDILRLGYTLAGHOKKILN	977
Qy	970	SIQVRAQNMNQISQVEV 986	
Db	978	SIQVRAQNMNQISQVEV 994	

Search completed: August 28, 2004, 04:12:52
 Job time : 98.1024 secs


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QY 421 SPQFASVNTTNOAPSAVSIMHOVSTVDSITLSMSQDPQNGVILDELOYEKEISE 480
DB 421 SPQFASVNTTNOAPSAVSIMHOVSTVDSITLSMSQDPQNGVILDELOYEKEISE 480
QY 481 YNATAISPTNTVVOGLKAGAIYVFOVARTAVAGRGYSGKXYPOTMTEAEVQTSIQEK 540
DB 481 YNATAISPTNTVVOGLKAGAIYVFOVARTAVAGRGYSGKXYPOTMTEAEVQTSIQEK 540
QY 541 LPLIGSSAAGVFLIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHWTGPKKIYIDPF 600
DB 541 LPLIGSSAAGVFLIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHWTGPKKIYIDPF 600
QY 601 TYEDPNAVAREFAKEIDISCVKIEOVYIAGEFGEVSGHLKLPKKEITVAITKLSGYT 660
DB 601 TYEDPNAVAREFAKEIDISCVKIEOVYIAGEFGEVSGHLKLPKKEITVAITKLSGYT 660
QY 661 EKORRDELSASIMGOFDHPNVTHLEBQVTKSTPVNIIEFEMENGLSDSFLRQNDGQFTV 720
DB 661 EKORRDELSASIMGOFDHPNVTHLEBQVTKSTPVNIIEFEMENGLSDSFLRQNDGQFTV 720
QY 721 IOVGMILRGIAAGMKYIADNMYVHRDLAARNILVNSNLVCYKSDPGLSFLSDPT 780
DB 721 IOVGMILRGIAAGMKYIADNMYVHRDLAARNILVNSNLVCYKSDPGLSFLSDPT 780
QY 781 TSAAGKIPRTWTAPEAIQYRKFTSASDVSYGIWMEVWSYGERPYMTNODVINAIE 840
DB 781 TSAAGKIPRTWTAPEAIQYRKFTSASDVSYGIWMEVWSYGERPYMTNODVINAIE 840
QY 841 QYRRLPPNDGSAHLQMLDQKQKRNHRPKGQIVNTLDKXIRNPSLKKAPLSSGI 900
DB 841 QYRRLPPNDGSAHLQMLDQKQKRNHRPKGQIVNTLDKXIRNPSLKKAPLSSGI 900
QY 901 NLPLDRTIPDYSFNTVDEMLEAIIKMGQYKESFAIAGFTSPDVVSQMMEDILRLGVTL 960
DB 901 NLPLDRTIPDYSFNTVDEMLEAIIKMGQYKESFAIAGFTSPDVVSQMMEDILRLGVTL 960
QY 961 AGHOKILNSIQVRAQMNQIOSVE 985
DB 961 AGHOKILNSIQVRAQMNQIOSVE 985

RESULT 2
ABU07847
ID ABU07847 standard; protein; 1055 AA.
XX
AC ABU07847;
XX
DT 10-MAY-2003 (first entry)
XX
DE Human ephrin receptor ligand EphB2.
XX
XX Cytostatic; vasodilator; antiinflammatory; cardiact; gene therapy;
XX ligand-receptor binding modulator; ephrin ligand; angiogenesis;
XX lymphangiogenesis; aberrant Ephrin-Tie biology; cell growth disorder;
XX cell migration disorder; cell proliferation disorder; neovascularisation;
XX ischemia; infarction; tissue graft; transplant; human;
XX ephrin receptor ligand; Tie receptor tyrosine kinase; EphB2.
XX
OS Homo sapiens.
XX
PN MO2003004529-A2.
XX
PD 16-JAN-2003.
XX
PF 02-JUL-2002; 2002WO-IB005224.
XX
PR 02-JUL-2001; 2001US-0302960P.
XX
PA (LIGN) LICENTIA LTD.
XX
PI Alicalo K, Kubo H;
XX
DB MPI; 2003-210341/20.

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DR N-PSDB; ABX12548.
XX
PT Identifying modulators of binding between a Tie receptor tyrosine kinase
PT and an Ephrin ligand, useful for promoting neovascularization, comprises
PT contacting a Tie receptor with an Ephrin in the presence of a putative
PT modulator.
XX
PS Disclosure; Page 128-132; 1999p; English.
XX
CC The invention describes a method of identifying a modulator of binding
CC between a Tie receptor tyrosine kinase and an Ephrin ligand. The method
CC comprises contacting a Tie receptor composition with an Ephrin
CC composition in the presence and in the absence of a putative modulator
CC compound, and detecting the binding between the receptor and the Ephrin
CC in the presence and in the absence of the putative modulator. The method
CC is useful for identifying a modulator of binding between a Tie receptor
CC tyrosine kinase and an Ephrin ligand. Modulators identified from the
CC method are useful in modulating angiogenic processes, including
CC lymphangiogenesis, for treating diseases associated with aberrant Ephrin-
CC Tie biology, aberrant growth, migration or proliferation of cells that
CC express a Tie receptor, or for promoting growth of vessel or
CC neovascularisation (e.g. ischemic tissue, an infarction, a new or
CC chronic compound, or a tissue graft or transplant). This is the amino
CC acid sequence of human EphB2, a member of the Ephrin-B subclass of
CC ligands that are bound to the membrane via a transmembrane domain and
CC short cytoplasmic tail and function as Ephrin receptor ligands
XX
SQ Sequence 1055 AA:
XX
Query Match 99.9%; Score 5181; DB 6; Length 1055;
XX
Best Local Similarity 99.9%; Pred. No. 0;
XX
Matches 984; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MALPRLGAILLPLLAARETLMDSTTATAEIGMWHPSGWEVSGYDENMTTRTYO 60
DB 1 MALPRLGAILLPLLAARETLMDSTTATAEIGMWHPSGWEVSGYDENMTTRTYO 60
QY 61 VCNVFESSQNNWLRTKFIERRGARHIVEMKFSVRDSSIPSPGSKETENLYYEADP 120
DB 61 VCNVFESSQNNWLRTKFIERRGARHIVEMKFSVRDSSIPSPGSKETENLYYEADP 120
QY 121 DSATKTFPNNMENPWWKVDITIADESFSQVDLGRVVKINTEVRSQPSRSGFYLAPOD 180
DB 121 DSATKTFPNNMENPWWKVDITIADESFSQVDLGRVVKINTEVRSQPSRSGFYLAPOD 180
QY 121 DSATKTFPNNMENPWWKVDITIADESFSQVDLGRVVKINTEVRSQPSRSGFYLAPOD 180
DB 121 DSATKTFPNNMENPWWKVDITIADESFSQVDLGRVVKINTEVRSQPSRSGFYLAPOD 180
QY 181 YGCGMSLIAVRVFRKCPRIIONGALFOETLSGAESTSLVAARGSCIANAEVDVPIKLY 240
DB 181 YGCGMSLIAVRVFRKCPRIIONGALFOETLSGAESTSLVAARGSCIANAEVDVPIKLY 240
QY 241 CNGDGEWLVPIGRCMKAGFEAVENTGVCRCGSPFKANQGDACHTCPINSRTTSEGA 300
DB 241 CNGDGEWLVPIGRCMKAGFEAVENTGVCRCGSPFKANQGDACHTCPINSRTTSEGA 300
QY 301 TNCYCRNGYRADLDPDMCTTIPSAPOAVISVNETSLMLEWTPRDSGGREDLYVNI 360
DB 301 TNCYCRNGYRADLDPDMCTTIPSAPOAVISVNETSLMLEWTPRDSGGREDLYVNI 360
QY 361 ICKSCSGGRGACTRCGDNVQYAPROGLTEPRYIIDLAHQYTFEIOAVNGVTDQSPF 420
DB 361 ICKSCSGGRGACTRCGDNVQYAPROGLTEPRYIIDLAHQYTFEIOAVNGVTDQSPF 420
QY 421 SPQFASVNTTNOAPSAVSIMHOVSTVDSITLSMSQDPQNGVILDELOYEKEISE 480
DB 421 SPQFASVNTTNOAPSAVSIMHOVSTVDSITLSMSQDPQNGVILDELOYEKEISE 480
QY 481 YNATAISPTNTVVOGLKAGAIYVFOVARTAVAGRGYSGKXYPOTMTEAEVQTSIQEK 540
DB 481 YNATAISPTNTVVOGLKAGAIYVFOVARTAVAGRGYSGKXYPOTMTEAEVQTSIQEK 540
QY 541 LPLIGSSAAGVFLIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHWTGPKKIYIDPF 600
DB 541 LPLIGSSAAGVFLIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHWTGPKKIYIDPF 600

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QY 601 TYEDPNEAVREPAKEIDISCVKIEOVIGAGEFGEVSGHKLPGKREIFAIAIKTLKSGYT 660
DB 601 TYEDPNEAVREPAKEIDISCVKIEOVIGAGEFGEVSGHKLPGKREIFAIAIKTLKSGYT 660
QY 661 EKQRDPFLSEASIMQGFDPHPNVIHLEGVYTKSPVMIITEFMENGSLSDFLRQNDGQFTV 720
DB 661 EKQRDPFLSEASIMQGFDPHPNVIHLEGVYTKSPVMIITEFMENGSLSDFLRQNDGQFTV 720
QY 721 IOLVGMRLGIAAGMYKYLADMYVHRLDLAARNILVNSNLVCYKSDFGLSRFLIEDTSDPT 780
DB 721 IOLVGMRLGIAAGMYKYLADMYVHRLDLAARNILVNSNLVCYKSDFGLSRFLIEDTSDPT 780
QY 781 TSALGCKTPIRWTAEALQYRKFTSASDVWSYGIWMEVWSYGERPYWDMNQDVINAIE 840
DB 781 TSALGCKTPIRWTAEALQYRKFTSASDVWSYGIWMEVWSYGERPYWDMNQDVINAIE 840
QY 841 QDYRLPPWDCPSALHQLMLDCMKDRNHRPKFGQIVNTLDMKIRPNLSKXMAPELSSGI 900
DB 841 QDYRLPPWDCPSALHQLMLDCMKDRNHRPKFGQIVNTLDMKIRPNLSKXMAPELSSGI 900
QY 901 NIPLDRTIPDYTSRNTVDENLEAIKMGYKESFANAGTSDVYSQMMEDILRLGVTTL 960
DB 901 NIPLDRTIPDYTSRNTVDENLEAIKMGYKESFANAGTSDVYSQMMEDILRLGVTTL 960
QY 961 AGHOKKILNSIQWRAQNNQIOSVE 985
DB 961 AGHOKKILNSIQWRAQNNQIOSVE 985
RESULT 3
AAB19590
ID AAB19590 standard; protein; 987 AA.
XX AAB19590;
XX 22-JAN-2001 (first entry)
XX Human CASB616.
XX CASB616; EPHB2; ERK; EPH3; EPH3; DRT; HEK5; EPHB2v;
XX receptor protein tyrosine kinase; human; antigen; colon cancer;
XX ovary cancer; tumour; autoimmune disease; vaccine; therapy; diagnosis.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Misc-difference 568..569
FT /note="an additional Arg residue decodes from the
FT CASB616 nucleotide sequence given in the specification
FT (see AAB8548), but is not given in the CASB616 amino
FT acid sequence in the specification"
FT Misc-difference 956
FT /note="encoded by GTT"
XX WO200053216-A2.
XX 14-SEP-2000.
XX 28-FEB-2000; 2000WO-EP001587.
XX 05-MAR-1999; 99GB-00005124.
XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX Vinals y De Baessolsc;
XX WPI: 2000-587384/55.
XX N-PSDB; AAB8548.
XX Vaccine composition for treating ovarian and colon cancer, comprises
PT CASB616 polypeptides, polynucleotides or antigen presenting cells
PT expressing the polypeptides.
XX

PS Claim 1; Page 41; 57pp; English.
XX The present sequence is that of human CASB616, a member of the EPH and
CC EPH-related family of receptor protein tyrosine kinases. CASB616 is also
CC known as EPHB2, ERK, EPH3, EPH3, DRT, HEK5 and EPHB2v. CASB616
CC polypeptides and polynucleotides are important immunogens for specific
CC prophylactic or therapeutic immunization against tumours, especially
CC colon cancer (claimed) and ovarian cancer. They are specifically
CC expressed or highly over-expressed in tumours compared to normal cells
CC and can thus be targeted by antigen-specific immune mechanisms leading to
CC destruction of the tumour cells. They can also be used to diagnose the
CC occurrence of tumour cells. Their inappropriate expression can also cause
CC an induction of autoimmune responses, which can be corrected through
CC vaccination using the CASB616 polypeptides or polynucleotides
XX Sequence 987 AA;
SQ
Query Match 99.8%; Score 5177.5; DB 3; Length 987;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 986; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MALRRGALILLPLAAVEETLMDSTTATAEIGMWHVPSGMEVSGYDENNTITRTYQ 60
DB 1 MALRRGALILLPLAAVEETLMDSTTATAEIGMWHVPSGMEVSGYDENNTITRTYQ 60
QY 61 VCNVFESSQNNWLRTKFIERRGARIRHVENKFSYRDCSSIPSYFGSKETFTNYYYBADF 120
DB 61 VCNVFESSQNNWLRTKFIERRGARIRHVENKFSYRDCSSIPSYFGSKETFTNYYYBADF 120
QY 121 DSATKTPNNMENNPNVVDITLADDESFSQYDLGRVKKINTEVRSFGFVRSRSGFYLAFO 180
DB 121 DSATKTPNNMENNPNVVDITLADDESFSQYDLGRVKKINTEVRSFGFVRSRSGFYLAFO 180
QY 121 DSATKTPNNMENNPNVVDITLADDESFSQYDLGRVKKINTEVRSFGFVRSRSGFYLAFO 180
DB 121 DSATKTPNNMENNPNVVDITLADDESFSQYDLGRVKKINTEVRSFGFVRSRSGFYLAFO 180
QY 181 YGCGMSLIAVRVFRKCPRIIIONGAIPOETLSGAEISTLVAARGSCIANAEVDVPIKLY 240
DB 181 YGCGMSLIAVRVFRKCPRIIIONGAIPOETLSGAEISTLVAARGSCIANAEVDVPIKLY 240
QY 241 CNGDGEMLVPIGRCMCAAGFEAVENGTVCGPSGFTKANOGBACHCPINSTTSEGA 300
DB 241 CNGDGEMLVPIGRCMCAAGFEAVENGTVCGPSGFTKANOGBACHCPINSTTSEGA 300
QY 301 TNCVCRNGYRADLDPDMPTTIPSAPOAVISSVNETSLMEWTPPRDSGREDLVYNI 360
DB 301 TNCVCRNGYRADLDPDMPTTIPSAPOAVISSVNETSLMEWTPPRDSGREDLVYNI 360
QY 361 ICKSGSGRGACTRCDGNVQYAPRQLGTEPRRIYISDLAHTQYTBEOAVNGVYTDOSP 420
DB 361 ICKSGSGRGACTRCDGNVQYAPRQLGTEPRRIYISDLAHTQYTBEOAVNGVYTDOSP 420
QY 421 SPQASVNTTNOAAPSAVSIIMHQSRTVDSITLSGQPOPNVILDYELQYKEKELSE 480
DB 421 SPQASVNTTNOAAPSAVSIIMHQSRTVDSITLSGQPOPNVILDYELQYKEKELSE 480
QY 481 YNATAIKSPNTTVVOGLKAGAIYFQYRARTVAGYRSGKMFQJTEAREYOTSIOEK 540
DB 481 YNATAIKSPNTTVVOGLKAGAIYFQYRARTVAGYRSGKMFQJTEAREYOTSIOEK 540
QY 541 LPLIIGSSAAGLVPLIAVVAIYCN-RRGFERADSEYTDLQHYTSGHMPGKAIYDP 599
DB 541 LPLIIGSSAAGLVPLIAVVAIYCN-RRGFERADSEYTDLQHYTSGHMPGKAIYDP 599
QY 600 FTYEDPNEAVREPAKEIDISCVKIEOVIGAGEFGEVSGHKLPGKREIFAIAIKTLKSGY 659
DB 600 FTYEDPNEAVREPAKEIDISCVKIEOVIGAGEFGEVSGHKLPGKREIFAIAIKTLKSGY 659
QY 661 TEKQRDPFLSEASIMQGFDPHPNVIHLEGVYTKSPVMIITEFMENGSLSDFLRQNDGQFT 720
DB 661 TEKQRDPFLSEASIMQGFDPHPNVIHLEGVYTKSPVMIITEFMENGSLSDFLRQNDGQFT 720
QY 720 VIOLVGMRLGIAAGMYKYLADMYVHRLDLAARNILVNSNLVCYKSDFGLSRFLIEDTSDPT 779
DB 720 VIOLVGMRLGIAAGMYKYLADMYVHRLDLAARNILVNSNLVCYKSDFGLSRFLIEDTSDPT 779
QY 779 VIOLVGMRLGIAAGMYKYLADMYVHRLDLAARNILVNSNLVCYKSDFGLSRFLIEDTSDPT 780
DB 779 VIOLVGMRLGIAAGMYKYLADMYVHRLDLAARNILVNSNLVCYKSDFGLSRFLIEDTSDPT 780

QY	780	YTSALGKGIPIRMTLPEAIIQYRKFTSADVWSYGIIVMEVWSYGERPYWMDTNOCVNAI	83		
Db	781	YTSALGKGIPIRMTLPEAIIQYRKFTSADVWSYGIIVMEVWSYGERPYWMDTNOCVNAI	840		
QY	840	EODYPLPPMDPCPSALHQLMTDCWQKDRNHRPKFGQIVNTLDMKIRPNPSIKAPAPLSSG	839		
Db	841	EODYPLPPMDPCPSALHQLMTDCWQKDRNHRPKFGQIVNTLDMKIRPNPSIKAPAPLSSG	900		
QY	900	INLPILDDITIPDYTSFNTFVDEMLELEIKMGQYKESFPANAGFTSPVVSQMMEDILRLGYT	955		
Db	901	INLPILDDITIPDYTSFNTFVDEMLELEIKMGQYKESFPANAGFTSPVVSQMMEDILRLGYT	960		
QY	960	LAGHOKKIILNSIQVRAQMNQIQSYEV	986		
Db	961	LAGHOKKIILNSIQVRAQMNQIQSYEV	987		
RESULT 4					
AAW26366					
ID	AAW26366	standard; protein; 994 AA.			
XX	AAW26366;				
AC					
XX					
DT	02-DEC-1997	(first entry)			
XX					
DE	Mouse Nuk tyrosine kinase.				
XX					
XX	Nuk tyrosine kinase; Eph receptor tyrosine kinase; signal transduction;				
XX	axoogenesis; neurodegenerative disease; Alzheimer's disease;				
KW	Parkinson's disease; Huntington's disease; multiple sclerosis;				
KW	amyotrophic lateral sclerosis; Wernicke's disease; nerve damage; trauma;				
KW	ischemia; stroke.				
OS	Mus musculus.				
XX					
XX					
FH	Key	Location/Qualifiers			
FT	Peptide	1..26			
FT		/label= Sig_peptide			
FT	Protein	27..994			
FT		/label= Mat_protein			
FT	Domain	27..548			
FT		/label= Extracellular_domain			
FT	Region	330..420			
FT		/label= FNIII			
FT		/note= "fibronectin type III repeat"			
FT	Region	444..534			
FT		/label= FNIII			
FT		/note= "fibronectin type III repeat"			
FT	Domain	549..574			
FT		/label= Transmembrane_domain			
FT	Domain	575..994			
FT		/label= Cytoplasmic_domain			
FT	Region	623..888			
FT		/label= Tyrosine-kinase_region			
XX					
XX	MO9714966-A1.				
XX					
PD	24-APR-1997.				
XX					
PF	10-OCT-1996;	96WO-CA000679.			
XX					
PR	13-OCT-1995;	95US-0005518P.			
XX					
XX	(MOUN) MOUNT SINAI HOSPITAL CORP.				
XX					
PI	Pawson A, Henkemeyer M;				
DR					
DR	WPI; 1997-245245/22.				
DR	N-FSDB; AAT84528.				
PT	Activation of ligand regulatory pathways by Eph subfamily receptor				
PT	tyrosine kinases - for stimulating or inhibiting axoogenesis, useful for				
PT	treatment of e.g. neurodegenerative diseases such as Alzheimer's or				

PT	Parkinson's diseases.
PS	Disclosure; Fig 3; 55bp; English.
XX	Murine Nuk tyrosine kinase is an Eph subfamily receptor tyrosine kinase that is essential for formation of the medial tract of the anterior commissure of the brain, and which appears to play a role in the formation of the habenular interpeduncular tract. Its amino acid sequence was deduced from cDNA clones (see A694528) isolated from an embryo cDNA library. The extracellular domain of Nuk was shown to be sufficient for formation of the medial tract. Eph subfamily receptor tyrosine kinases (e.g. the Nuk extracellular domain) can be used in claimed methods to:
CC	activate a ligand regulatory pathway in a cell; identify substances able to bind a ligand for an Eph subfamily receptor tyrosine kinase; and to affect neuronal development or regeneration, especially the stimulation or inhibition of axonogenesis, in a mammal. Activation of the ligand regulatory pathway results in downstream activation of a series of:
CC	cytoskeletal architecture, cell metabolism, cell migration and cell-cell interactions. Substances which activate the ligand regulatory pathway may be used for stimulating or inhibiting neuronal development regeneration and axonal migration associated with neurodegenerative disease e.g. Alzheimer's, Parkinson's or Huntington's diseases, multiple sclerosis, amyotrophic lateral sclerosis, deficiency diseases such as Wernicke's disease, peripheral nerve damage, trauma and ischaemia resulting from stroke
CC	
XX	
SQ	Sequence 994 AA;
Query Match	98.9%; Score 5130; DB 2; Length 994;
Best Local Similarity	99.5%; Pred. No. 0;
Matches 972; Conservative	4; Mismatches 1; Indels 0; Gaps 0
OY	10 LLLPLLAABEETLMDSTTATAELGMMVHPSPSGMEVSIGYEDNMTITTYOVCNVFSSQ 69
DB	18 LLLPLLAABEETLMDSTTATAELGMWVHPPSGMEEVSGYEDNMNTITTYOVCNVFSSQ 77
OY	70 NNMLRTKRIIRRGAGARIHVEMKFVRDCCIISPVSGCKETFNLYYYEADPDSATKTPN 129
DB	78 NNMLRTKRIIRRGAGARIHVEMKFVRDCCIISPVSGCKETFNLYYYEADPDLAKTPN 137
OY	130 WMENPWVKVDITLAADESFQVDLGGRVKIKITEVRSFGVPVSRSGFYLAFOYGCGMSLIA 189
DB	138 WMENPWVKVDITLADESFQVDLGGRWKIKITEVRSFGVPVSRNGFYLAFOYGCGMSLIA 197
OY	190 VRVRYRKCPRIIIONGAIFOEITLSAESTSLVAARGSCTIANAEVDVPIKLXCNGBEWLV 249
DB	198 VRVRYRKCPRIIIONGAIFOEITLSAESTSLVAARGSCTIANAEVDVPIKLXCNGBEWLV 257
OY	250 PIGRCMKAGEAVENGTVGRGCSSGFIFKANQGDACTHCPIINRSTTSSEGANVCYCRRGY 309
DB	258 PIGRCMKAGEAVENGTVGRGCSSGFIFKANQGBEACTHCPIINRSTTSSEGANVCYCRRGY 317
OY	310 YRALDLPELMPCTTIIPSAPOAVISVNSETSLMLETPRPDGSGREDLYNNITICKSCGSGR 369
DB	318 YRALDLPELMPCTTIIPSAPOAVISVNSETSLMLETPRPDGSGREDLYNNITICKSCGSGR 377
OY	370 GACTRCGDNVQYAPROQLGLEPRIIYSIDLLAHITOYTEFIQAVNGVTQDSPSPQASVINI 429
DB	378 GACTRCGDNVQYAPROQLGLEPRIIYSIDLLAHITOYTEFIQAVNGVTQDSPSPQASVINI 437
OY	430 TTINAASAVSINHMOVSRIVDSITLSMSOPDPQPGVILLDELQYKEKLSFYNNATIXSP 489
DB	438 TTINAASAVSINHMOVSRIVDSITLSMSOPDPQPGVILLDELQYKEKLSFYNNATIXSP 497
OY	490 TINTVVOGLKAGAIYVEQVARIVAGYGRYSGMYFOPTMTAEAYOTSIOEKLPILIGSSA 549
DB	498 TINTVVOGLKAGAIYVEQVARIVAGYGRYSGMYFOPTMTAEAYOTSIOEKLPILIGSSA 557
OY	550 AGLEVFLIAVVVIAIVCNRGRFEARDSYTKLOHYNSGHMTPGKKIYIIDPPTYDPAEAV 609
DB	558 AGLEVFLIAVVVIAIVCNRGRFEARDSYTKLOHYNSGHMTPGKKIYIIDPPTYDPAEAV 617

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QY 610 REFKEIDISCVKIEGVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORRDELS 669
|
|
|
Db 618 REFKEIDISCVKIEGVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORRDELS 677
|
|
|
QY 670 EASIMQGFPHPNVTHLEGVVTKSTPMTTTEMENENSLDSPRLKQDGGCTTVQLVGMKLRG 729
|
|
|
Db 678 EASIMQGFPHPNVTHLEGVVTKSTPMTTTEMENENSLDSPRLKQDGGCTTVQLVGMKLRG 737
|
|
|
QY 730 IAAGMKYLAADNMYVHRDLAARNILVNSNLVCKVSPFGLSRPLEDDTSDPTYSALGKLP 789
|
|
|
Db 738 IAAGMKYLAADNMYVHRDLAARNILVNSNLVCKVSPFGLSRPLEDDTSDPTYSALGKLP 797
|
|
|
QY 790 IEMTAPBEALQYRKFTSASDVMSYGIYMAEVMASGERPYDMTNQDYINAIIEODYRLPPPM 849
|
|
|
Db 798 IEMTAPBEALQYRKFTSASDVMSYGIYMAEVMASGERPYDMTNQDYINAIIEODYRLPPPM 857
|
|
|
QY 850 DCPSSALHQLMLDCMQKDRNHRPEFGQIVNTLDMKIMNPNSLKAMAPLSSGINKLPDDRPI 909
|
|
|
Db 858 DCPSSALHQLMLDCMQKDRNHRPEFGQIVNTLDMKIMNPNSLKAMAPLSSGINKLPDDRPI 917
|
|
|
QY 910 PDYTSFNTVDLWLEAIKMGQYKESFANAGFTSPDVVSQMMEDILRLGVTLAHOQKILN 969
|
|
|
Db 918 PDYTSFNTVDLWLEAIKMGQYKESFANAGFTSPDVVSQMMEDILRLGVTLAHOQKILN 977
|
|
|
QY 970 SIOWMAQONNOIOSVEV 986
|
|
|
Db 978 SIOWMAQONNOIOSVEV 994
|
|
|

RESULT 5
AAU01907
ID AAU01907 standard; protein; 994 AA.
XX
AC AAU01907;
XX
DT 29-AUG-2001 (first entry)
XX
DE Murine neural kinase (Nuk) polypeptide.
XX
XX Neural kinase; Nuk; receptor tyrosine kinase; axonal migration; stroke;
XX nerve fibre; cell-cell interaction; axonogenesis; neuronal development;
XX regeneration; neurodegenerative disorder; Alzheimer's disease; ischaemia;
XX Parkinson's disease; Huntington's disease; demyelinating disease;
XX multiple sclerosis; amyotrophic lateral sclerosis; deficiency disease;
XX Werner's disease; nutritional polyneuropathy; multistep degeneration;
XX progressive supranuclear palsy; Shy Drager's syndrome; mouse;
XX olivoponto cerebellar atrophy; peripheral nerve damage.
XX
XX Mus musculus.
XX
FH Key Location/Qualifiers
FT 1..26 /note="Signal peptide"
FT 26..548 /note="Extracellular domain, preferably residues 26-544"
FT Domain
FT Protein
FT 27..994 /note="Mature murine neural kinase"
FT 52..119 /note="Ig-like domain"
FT Domain
FT 239..268 /note="Ig-like domain"
FT Region
FT 330..420 /note="Ig-like Nuk repeat"
FT Region
FT 444..534 /note="Fibronectin type III repeat"
FT Region
FT 549..574 /note="Fibronectin type III repeat"
FT Domain
FT 600..618 /note="Hydrophobic transmembrane domain"
FT Binding-site
FT 601..994 /note="SH2 domain binding site"
FT Region
FT 604 613 /note="Carboxy terminal"
FT Modified-site
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FT Domain 623..888
|
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|
FT Binding-site /note="Catalytic tyrosine kinase domain"
FT 623..707
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|
FT /note="ATP binding site"
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|
US6218356-B1.
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PD 17-APR-2001.
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|
PR 13-OCT-1995; 95US-00542635.
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PR 29-APR-1994; 94US-00235407.
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|
PR 28-APR-1995; 95MO-CA000254.
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(MOUN ) MOUNT SINAI HOSPITAL CORP.
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Pawson A, Henkemeyer M, Lewin K;
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MPI; 2001-289845/30.
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|
DR N-PSDB; AAS03812.
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|
New composition comprising neural receptor tyrosine kinase protein useful
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|
PT for inhibiting or stimulating axonogenesis, neuronal development, or
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|
PT regeneration and axonal migration.
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PS Claim 1; Fig 2; 86pp; English.
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|
XX The sequence represents a mouse neural kinase (Nuk) polypeptide. The
XX murine Nuk locus has been mapped to the distal end of chromosome four.
XX The polypeptide is a novel receptor tyrosine kinase protein, and is found
XX to be expressed at high levels within migrating axons and is associated
XX with nerve fibres. It functions to regulate specific cell-cell
XX interactions during early development of the nervous system and in
XX axonogenesis. Substances which bind to the Nuk protein, particularly
XX ligands, may be used for stimulating or inhibiting neuronal development,
XX regeneration and axonal migration associated with neurodegenerative
XX disorders and conditions involving trauma and injury to the nervous
XX system. These disorders include Alzheimer's disease, Parkinson's disease,
XX Huntington's disease, demyelinating diseases such as multiple sclerosis,
XX amyotrophic lateral sclerosis, deficiency diseases such as Werner's
XX disease and nutritional polyneuropathy, progressive supranuclear palsy,
XX Shy Drager's syndrome, multistep degeneration, olivoponto cerebellar
XX atrophy, peripheral nerve damage, and ischaemia resulting from stroke.
XX The proteins may be used to prepare antibodies having specificity for Nuk
XX proteins, which can be used to diagnose or treat disorders of the nervous
XX system. These proteins are also used for screening agonists or
XX antagonists of the interactions of the Nuk proteins with binding
XX molecules
XX
XX
XX Sequence 994 AA:
XX
XX
XX Query Match 98.9%; Score 5130; DB 4; Length 994;
XX Best Local Similarity 99.5%; Pred. No. 0;
XX Matches 972; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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|
QY 10 LLLPLLAAVEETLMDSTTATLALGKMYHPSPSGMEVSGYDENNNITRTYVCVAVPSSQ 69
|
|
|
Db 18 LLLPLLAAVEETLMDSTTATLALGKMYHPSPSGMEVSGYDENNNITRTYVCVAVPSSQ 77
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|
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QY 70 NNWLRTKFTIRRRGARIRIVEKFSVRDOCSIPSPSGCKETFNLYYEADSDATKTFPN 129
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|
|
Db 78 NNWLRTKFTIRRRGARIRIVEKFSVRDOCSIPSPSGCKETFNLYYEADSDATKTFPN 137
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|
|
QY 130 WKENPWKVDTTIAADESFQVDLGRVWKINTVEVRSFGPVRSRGPYLAFDYGGCMSTIA 189
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Db 138 WKENPWKVDTTIAADESFQVDLGRVWKINTVEVRSFGPVRSRGPYLAFDYGGCMSTIA 197
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|
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QY 190 VRVFRKCPRIIOGATFOETLSGAEISTVAAAGSCIANAEVDVPIKLYCNGDGEMLV 249
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|
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Db 198 VRVFRKCPRIIOGATFOETLSGAEISTVAAAGSCIANAEVDVPIKLYCNGDGEMLV 257
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QY 250 PIGRCMKAGAEAVENGTVGCGSPGTFKANKQGDGACTHCPINERTTSEGATNCVCENGY 309
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Db 258 PIGRCMKAGFEAVENGTVGRCPSGTFKXANQDDEACTHCPINSRTTSGATNCVRNGY 317
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 Db 318 YRADLDLDMPCCTTISAPQAVISSVNETSIMLEMPPPRSGREDLVNIIICKSGSGR 377
 QY 370 GACTRCGDNYQYAPROGLTEPRITISDLAHTQYFEIQAQVAVTDOSEFSPQFASVNI 429
 Db 378 GACTRCGDNYQYAPROGLTEPRITISDLAHTQYFEIQAQVAVTDOSEFSPQFASVNI 437
 QY 430 TTNOAASAVSINHQSRTVDSITLSWSQDPOQNGVILDELOYEKEJSEYNATIKSP 489
 Db 438 TTNOAASAVSINHQSRTVDSITLSWSQDPOQNGVILDELOYEKEJSEYNATIKSP 497
 QY 490 TMTVTGGLKAGAIYVQVAPARTVAGYGRYSGMYQTMTEARYQCSIOEKLPLIIGSSA 549
 Db 498 TMTVTGGLKAGAIYVQVAPARTVAGYGRYSGMYQTMTEARYQCSIOEKLPLIIGSSA 557
 QY 550 AGVFLIAVVVIAIVCNRGRFEPADSEYTDKLOHYTSGHMTFGMKIYIDPFYEDNEAV 609
 Db 558 AGVFLIAVVVIAIVCNRGRFEPADSEYTDKLOHYTSGHMTFGMKIYIDPFYEDNEAV 617
 QY 610 REFAPKEIDISCVAIEQVIGAGEFGEVCSGHLKPGKREIFVAIKTLKSGYTEKORDELS 669
 Db 618 REFAPKEIDISCVAIEQVIGAGEFGEVCSGHLKPGKREIFVAIKTLKSGYTEKORDELS 677
 QY 670 EASIMQGFDPHPNIIIEGVVTKSTPVMIITEFMENGLSDSFLRQNDGQFTVIQVGMIMG 729
 Db 678 EASIMQGFDPHPNIIIEGVVTKSTPVMIITEFMENGLSDSFLRQNDGQFTVIQVGMIMG 737
 QY 730 IAAQMKYLAQMYVHRPLAARNTLVNSNLVCKYSDGSLRFLDDPDSPTYSALGKRP 789
 Db 738 IAAQMKYLAQMYVHRPLAARNTLVNSNLVCKYSDGSLRFLDDPDSPTYSALGKRP 797
 QY 790 IRTAPEAIQYRKFTSASDVMSYGIWMEVMSYGERPYMDMTQDINAIEDYRLPPM 849
 Db 798 IRTAPEAIQYRKFTSASDVMSYGIWMEVMSYGERPYMDMTQDINAIEDYRLPPM 857
 QY 850 DCSALHQLMDQWQDRNHRPRFGQIVNTLDMKINPNSLKAMAPLSSGINLPLIDRTI 909
 Db 858 DCSALHQLMDQWQDRNHRPRFGQIVNTLDMKINPNSLKAMAPLSSGINLPLIDRTI 917
 QY 910 PDYTSFNTVDENLEAIKMGQYKESFANAGTSDVVSQMMEDILEGVTLAGHOKKILN 969
 Db 918 PDYTSFNTVDENLEAIKMGQYKESFANAGTSDVVSQMMEDILEGVTLAGHOKKILN 977
 QY 970 SIOVMAQNNQIOSVEV 986
 Db 978 SIOVMAQNNQIOSVEV 994
 RESULT 6
 AAR87018 standard; protein; 994 AA.
 ID AAR87018;
 AC AAR87018;
 XX
 DT 19-MAR-1996 (first entry)
 XX
 DE Receptor tyrosine kinase (neural kinase).
 XX
 KW Receptor tyrosine kinase; neural kinase; Nuk; axon; axonogenesis;
 XX
 KW nerve disorder.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT 1..26
 FT /label= Sig_peptide
 FT 27..548
 FT /label= Extracellular region
 FT /note= "the extracellular region (amino acids 27-548)
 FT includes an N-terminal Ig-like domain and an Ig-like Nuk

FT FT repeat
 FT Region 330..420
 FT /label= FNIII
 FT /note= "fibronectin type III repeat"
 FT Region 444..534
 FT /label= FNIII
 FT /note= "fibronectin type III repeat"
 FT Region 549..574
 FT /label= Transmembrane_region
 FT Region 575..994
 FT /label= Cytoplasmic_region
 FT Domain 623..707
 FT /label= Tyrosine-kinase_catalytic_domain
 FN MO9530326-A1.
 XX
 PD 09-NOV-1995.
 XX
 PF 28-APR-1995; 95WD-CA000254.
 XX
 PR 29-APR-1994; 94US-00235407.
 XX
 PA (MOUN) MOUNT SINAI HOSPITAL CORP.
 PI Pawsan A, Henkemeyer M, Letwin K;
 XX
 DR WPI, 1995-393299/50.
 DR N-PSDB; AAT07308.
 XX
 PT DNA encoding neural receptor tyrosine kinase - useful in gene therapy of
 PT nerve disorders, and for diagnosis and identification of therapeutic
 PT agents.
 PS Claim 1; Page 70-74; 103pb; English.
 CC A novel receptor tyrosine kinase (AAR87018), designated neural kinase
 CC (Nuk) (AAR87018), is encoded by cDNA (AAT07308) obtd. from a mouse embryo
 CC library. Nuk is expressed in migrating axons and is involved in cell-cell
 CC interactions and axonogenesis in development of the nervous system. Nuk
 CC or its fragments (pref. amino acids 26-548 or 501-994) are used to
 CC identify (ant)agonists of the (activated) receptor tyrosine kinase as a
 CC means of treating nerve disorders and damage, or to raise antibodies used
 CC to monitor axon migration and nerve cell interactions
 XX
 SQ Sequence 994 AA:
 Query Match 98.8%; Score 5126; DB 2; Length 994;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 971; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 QY 10 LLLPLLAAYEETLMDSTTATAEIGMMVHPSPGMEVSGYDENMNTIRTYQCVNFESSQ 69
 Db 18 LLLPLLAAYEETLMDSTTATAEIGMMVHPSPGMEVSGYDENMNTIRTYQCVNFESSQ 77
 QY 70 NNWLRTKFIIRRGGAHRIHVEKFSVRDSSIPSPGSCKETENLYYYEADFDSATKTFPN 129
 Db 78 NNWLRTKFIIRRGGAHRIHVEKFSVRDSSIPSPGSCKETENLYYYEADFDSATKTFPN 137
 QY 130 WNEPWYKVDITIADESFSQVDIGRVMKINTVRSRGPYSRSGFYLAPODYGCGSLTA 189
 Db 138 WNEPWYKVDITIADESFSQVDIGRVMKINTVRSRGPYSRSGFYLAPODYGCGSLTA 197
 QY 190 VRVFRKCPRIIONGAIFOETLSGABSTSLVAARGSCIANAEVDVPIKLYCNGDSEWLY 249
 Db 198 VRVFRKCPRIIONGAIFOETLSGABSTSLVAARGSCIANAEVDVPIKLYCNGDSEWLY 257
 QY 250 PIGRCMKAGFEAVENGTVGRCPSGTFKXANQDDEACTHCPINSRTTSGATNCVRNGY 309
 Db 258 PIGRCMKAGFEAVENGTVGRCPSGTFKXANQDDEACTHCPINSRTTSGATNCVRNGY 317
 QY 310 YRADLDLDMPCCTTISAPQAVISSVNETSIMLEMPPPRSGREDLVNIIICKSGSGR 369
 Db 318 YRADLDLDMPCCTTISAPQAVISSVNETSIMLEMPPPRSGREDLVNIIICKSGSGR 377

OY		370	GACRCDCDNOVAPRQGLTEPRITYSDLLATQYTFELQAVNGVTDSPPSPQASVNI	4289			
Db		378	GACRCGCDNQVAPRQLGLEPRIIYSDDLATHQVTFELQAVNGVTDSPPSPQASVNI	4378			
OY		430	TTTQAASAANSIMHQVSRTVDSTLTLSNSOPDPONGVILDYELQYIEKSLSYNATLKSP	4689			
Db		438	TTTQAASAANSIMHQVSRTVDSTLTLSMSQPDOPNGVIDYELQYIEKSLSEYNATAIKSP	4978			
OY		490	TNTYTQGLKAGAIYFQVVARPTVAGRGYSGKWTFQMTAEAYOTSIOEKLPIIISSA	5494			
Db		498	TNTYTQGLKAGAIYFYQVBARPTVAGRYSGKWFQMTAEAYOTSIOEKLPIIVSSA	5578			
OY		550	AGLVELIAVVVIAIVCNRRGFESADSEYTDKIQHITSGMTPGMKIYYIDPTYEDPNEAV	6098			
Db		558	AGLVFLIAVVVIAIVCNRRGFESADEYTDKIQHYTSGMTPGMKIYYIDPTYEDPNEAV	6178			
OY		610	REFAKEIDISCVAIKEOVI GAGEFGECSHLALPKREIFVAIKTLKSYTEKORPDFLS	6668			
Db		618	REFAKEDI SCVAIKEOVI GAGEFGEC SHLALPKREIFA IKT LKSGYTEKORPDFLS	6778			
OY		670	EASIMGOFDPHNVIHLBGVTKSTPVMIITTEMENGSLDSPLRONDQGFVIIQLVGMLRG	7298			
Db		678	EASIMGOFDPHNVIHLGGVTKSTPVMIITTEMENGSLDSPLRONDQGFVIIQLVGMLRG	7378			
OY		730	IAGMKTALAMNVYHDDLAARNILVNSNLVCVKSPGSLRFLEDPTSDFPYTSA LGKIP	7898			
Db		738	IAGMKTALAMNVYHDDLAARNILVNSNLVCVKSPGSLRFLEDPTSDFPYTSA LGKIP	7978			
OY		790	IRWTPAPAIOYRKFTSASDVWSYGI VMEWVS YGERPFWDMTNDQVINALEODYRLPEPM	8498			
Db		798	IRWTPAPAIOYRKFTSASDVWSYGI VMEWVS YGERPFWDMTNDQVINALEODYRLPEPM	8578			
OY		850	DCPSALHQLMLDCWKDRNRHPKFGQIVNTLDKMI RNPNLSKAPAPLSSGILNPLDRTI	9098			
Db		858	DCPSALHQLMLDCWKDRNRHPKFGQIVNTLDKMI RNPNLSKAPAPLSSGILNPLDRTI	9178			
OY		910	PDYTSSENTVDWELEAIKMGYKESFPANAGFTSFDDVASCMMMEDILRLGVTLAGHKIILN	9688			
Db		918	PDYTSSENTVDWELEAIKMGYKESFPANAGFTSFDDVASCMMMEDILRVGVTLAGHKIILN	9778			
OY		970	SIOVMRAQNQIOSVEY 986				
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RESULT 7							
AA85089							
ID	AA85089	standard; protein; 970 AA.					
XX							
AC	AA85089;						
XX							
DT	16-APR-1996	(first entry)					
XX							
DE	EPH-like receptor protein tyrosine kinase HEK5.						
XX							
KW	EPH-like receptor protein tyrosine kinase: PTK; HEK5;						
XX	human eph-like kinase; therapy; diagnosis; vector; antibody.						
OS	Homo sapiens.						
XX							
FN	W0528484-A1.						
XX							
PD	26-OCT-1995.						
XX							
PF	14-APR-1995;	95MO-US004681.					
XX							
PR	15-APR-1994;	94US-00229509.					
XX							
PA	(AMGE-) AMGEN INC.						
XX							
DI	Fox GM, Welcher AA, Jing S;						

Query Match	Best Local Similarity	98.2%	Score 5093;	DB 2;	Length 970;
Matches	967;	Conservative	2;	Mismatches	1;
				Indels	2;
				Gaps	1
QY	15	LLAAVEELTMSTATAELGMMVHPSPGMEVSGYDENNTIRTYQVCNVFESSQNNMLR	74		
Db	1	LLAAVEELTMSTATAELGMMVHPSPGMEVSGYDENNTIRTYQVCNVFESSQNNMLR	60		
QY	75	TKTIRRRGARRIHVEMKFSVDDCSIPSPGSKETFMLYYYEADFDSATKTFENWMENP	134		
Db	61	TKTIRRRGARRIHVEMKFSVDDCSIPSPGSKETFMLYYYEADFDSATKTFENWMENP	120		
QY	135	WVKVDTLIAADSFGQVLDGGRVYKINTEVRSPGYSRSGFLAPQDYGCGMSLIYARIFY	194		
Db	121	WVKVDTLIAADSFGQVLDGGRVYKINTEVRSPGYSRSGFLAPQDYGCGMSLIYARIFY	180		
QY	195	RKCPRIIIONGAIPOETLSGAESTLSVAARGSCIANAEEDVPKILYKNGDGMVLPIGRG	254		
Db	181	RKCPRIIIONGAIPOETLSGAESTLSVAARGSCIANAEEDVPKILYKNGDGMVLPIGRG	240		
QY	255	MCKGFEVKEVGYTCRGPGSGTFEFGANGDEACTHCPIINSRTTSBATNCVCRNGYYRDL	314		
Db	241	MCKGFEVKEVGYTCRGPGSGTFEFGANGDEACTHCPIINSRTTSBATNCVCRNGYYRDL	300		
QY	315	DPLDMPCTTISAPQAQVAIVSSVNEISLMEMTPRPSDGSREDLVYNIICKSGSGRGACTR	374		
Db	301	DPLDMPCTTISAPQAQVAIVSSVNEISLMEMTPRPSDGSREDLVYNIICKSGSGRGACTR	360		
QY	375	CGENVQIAPROLGLTEPRITYSDLLAHTQYTFEIOAVNGVTDQSFSPSQFASVNTTNOA	434		
Db	361	CGENVQIAPROLGLTEPRITYSDLLAHTQYTFEIOAVNGVTDQSFSPSQFASVNTTNOA	420		
QY	435	APSAVSIMHQVSRATVDSITLSMSOPDPQNGVILDELOYEKEISEVYATAIKSPNTNYT	494		
Db	421	APSAVSIMHQVSRATVDSITLSMSOPDPQNGVILDELOYEKEISEVYATAIKSPNTNYT	480		
QY	495	VQGLKAGAIYFQVPARTVAGYGRYSKMYFQMTAEAYQTSIQEKLPLITIGSSAAGLVF	554		
Db	481	--GLKAGAIYFQVPARTVAGYGRYSKMYFQMTAEAYQTSIQEKLPLITIGSSAAGLVF	538		
QY	555	LIAVVAIAIVCNRRGFERADSEYTDKIOHYSNGHMPKMTIYIDPFTYEDPNEAVREFAK	614		
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QY	615	EIDISCVKIEQVIGAGEFEVYSGHKLKPGKREIIVAIKITLKSQYTEKORDPJLSEASIM	674		
Db	599	EIDISCVKIEQVIGAGEFEVYSGHKLKPGKREIIVAIKITLKSQYTEKORDPJLSEASIM	658		

DT 25-MAR-2003 (revised)
DT 11-NOV-1995 (first entry)
XX Eph-related PTK Cdk5+.
XX Cdk5+, Eph; protein tyrosine-kinase; PTK; cancer; diagnosis; prognosis.
XX Gallus sp.
XX MO9515375-A1.
XX 08-JUN-1995.
XX 07-SEP-1994; 94MO-US010140.
XX 03-DEC-1993; 93US-00162809.
XX (LJOL-) LA JOLIA CANCER RES FOUND.
XX Pasquale EB, Sajjadi FG;
XX WPI, 1995-215256/28.
XX N-PSDB; AAQ90657.
XX Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing
XX cancer.
XX Claim 11, Page 71-75; 129pp; English.
XX A cDNA clone encoding a novel variant of Eph-related PTK Cdk5, Cdk5+
XX (AAQ90657), was isolated from a chick embryo library in lambda g11.
XX Cdk5+ protein (AA875709) contains a 16-amino acid insertion in the
XX juxtamembrane domain, and be a result of alternative splicing. Cdk5+ is
XX exclusively expressed in the CNS. (Updated on 25-MAR-2003 to correct PN
XX field.)
XX Sequence 1011 AA;
SQ

Query Match 95.8%; Score 4971.5; DB 2; Length 1011;
Best Local Similarity 94.2%; Pred. No. 0;
Matches 936; Conservative 29; Mismatches 12; Indels 17; Gaps 2;

QY 10 LLLPLIAAEEITLMDSTIAELGMMVHPSPGMEEVSGYDENMTIRTYQVCNPFSSQ 69
DB 18 LALLPLIAAEEITLMDSTIAELGMMVHPSPGMEEVSGYDENMTIRTYQVCNPFSSQ 77
QY 70 NMLRTKFIIRRGHRIHVMKFSVSDCSIPSPGCKETFNLYYYEADPDSATKTFPN 129
DB 78 NMLRTKFIIRRGHRIHVMKFSVSDCSIPSPGCKETFNLYYYEADPDSATKTFPN 137
QY 130 WMENPWKVDITIADESFQVDLGRVYKINTEVRSFPGVRSRGLAFQDYGGMSLIA 189
DB 138 WMENPWKVDITIADESFQVDLGRVYKINTEVRSFPGVRSRGLAFQDYGGMSLIA 197
QY 190 VRFYFRKCPRIIONGALFQETLSGABESTLVAARGSCIANAEVDVPIKLYCNGDEMLV 249
DB 198 VRFYFRKCPRIIONGALFQETLSGABESTLVAARGSCIANAEVDVPIKLYCNGDEMLV 257
QY 250 PIGRCMKAGFEAVENGTVRGCPSTGFKANOGDEACTHCPINSRTTSEGATNCVCRNGY 309
DB 258 PIGRCMKRPFESYENGTGRCGSGTFKASQGBECVHCPIINSRTTSEGATNCVCRNGY 317
QY 310 YRADLDPLDMPCTTIPAPAVISSVNETSLMLEMTPRDSGREDLVNIIKSCSGSR 369
DB 318 YRADLDPLDMPCTTIPAPAVISSVNETSLMLEMTPRDSGREDLVNIIKSCSGSR 377
QY 370 GACTRCGDNQYAFRQGLTEPRYIISDLLAHQYTFEIQAVNGVTLDSFPSPQFASVNI 429
DB 378 GACTRCGDNQYAFRQGLTEPRYIISDLLAHQYTFEIQAVNGVTLDSFPSPQFASVNI 437
QY 430 TTNOAPSAVSIHQVSRVTDSITLSWSQPDQNGVILDYELQYKEKLESYNAITAKSP 489
DB 438 TTNOAPSAVSIHQVSRVTDSITLSWSQPDQNGVILDYELQYKEKLESYNAITAKSP 497

QY 490 TINTVVOGLKAGATVYQVARTVAGYGRYSKKRYFQTMTEAEYQTSIOEKLPIIGSSA 549
DB 498 TINTVVOGLKAGATVYQVARTVAGYGRYSKKRYFQTMTEAEYQTSIOEKLPIIGSSA 557
QY 550 AGLVFLIAVVIATVYCN-RSGFERADSEYTDKLOHYTSGH-----MTPG 592
DB 558 AGLVFLIAVVIITVYCNRRRGFERADSEYTDKLOHYTSGHSTYGRPPGLGVRSLFPTPG 617
QY 593 MKIYIDPFTYEDPNEAVREFAKEIDICVKIEQYIGAGEFGEVCSGHUKLPKREIFVAI 652
DB 618 MKIYIDPFTYEDPNEAVREFAKEIDICVKIEQYIGAGEFGEVCSGHUKLPKREIFVAI 677
QY 653 KTLKSGYTEKORRDPFLSEASIMGOFDHPNVIHLEGVTKSTPPVITTEPMENSLDSFLR 712
DB 678 KTLKSGYTEKORRDPFLSEASIMGOFDHPNVIHLEGVTKSTPPVITTEPMENSLDSFLR 737
QY 713 QNDGQFTVIOVGMRLRGIAAGMKYIADNMYVHRDLAARNIIVNSNLVCKVSDFGLSRPLE 772
DB 728 QNDGQFTVIOVGMRLRGIAAGMKYIADNMYVHRDLAARNIIVNSNLVCKVSDFGLSRPLE 797
QY 773 DDTSDPTYSALGKIPIRMTAPBAIQYRKFTSADVWSYGIWMEVWSYGERPYMDNTN 832
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QY 833 QDVINAIEQDYRLPFPMDCPALHQLMLDCWQKXDRNHRPKFGQIVNTLDKXIRNPNLSIKA 892
DB 858 QDVINAIEQDYRLPFPMDCPALHQLMLDCWQKXDRNHRPKFGQIVNTLDKXIRNPNLSIKA 917
QY 893 MAPLSSGYNLPLDRTIPDYTSFNTVDENLEAIKMGQYKESFANAFTSPVNSQMMED 952
DB 918 MAPLSSGYNLPLDRTIPDYTSFNTVDENLEAIKMGQYKESFANAFTSPVNSQMMED 977
QY 953 ILRLGVTLAGHOKTILNSIQVRAQNMQIQSVEV 986
DB 978 ILRLGVTLAGHOKTILNSIQVRAQNMQIQSVEV 1011

Search completed: August 28, 2004, 04:08:44
Job time : 100.585 secs

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GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: August 28, 2004, 03:50:54 ; Search time 19.6423 Seconds
(without alignments)
2796.715 Million cell updates/sec

Title: US-09-914-883-4
Perfect score: 5571
Sequence: 1 MALRRIGALLPLLAAYE.....QGIFKEDSHKESNDCGCG 1055

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 90%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	5568	99.9	1055 1 EPHB2_HUMAN	P29323 homo sapien
2	5129	92.1	994 1 EPHB2_MOUSE	P54763 mus muscul

ALIGNMENTS

RESULT 1
EPHB2_HUMAN
ID EPHB2_HUMAN STANDARD; PRT; 1055 AA.
AC P29323; O43477;
DT 01-DEC-1992 (Rel. 24, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ephrin type-B receptor 2 precursor (EC 2.7.1.112) (Tyrosine-protein
kinase receptor EPH-3) (DRT) (Receptor protein-tyrosine kinase HEK5
(ERK)).
GN EPHB2 OR EPH3 OR ERK OR DRT OR HEK5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_Taxid=9606;
CX [1]
RN SEQUENCE FROM N.A. (ISOFORM SHORT).
RC TISSUE=Fetal brain;
RX MEDLINE=96154673; PubMed=8589679;
RA Ikegaki N., Tang X.X., Liu X.-G., Biegel J.A., Allen C.,
RA Yoshida A., Sultan E.P., Brodeur G.M., Pleasure D.B.,
RT "Molecular characterization and chromosomal localization of DRT
RT (EPH3): a developmentally regulated human protein-tyrosine kinase
RT gene of the EPH family.";
RL Hum. Mol. Genet. 4:2033-2045(1995).
[2]

RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RC TISSUE=Gastric carcinoma;
RX MEDLINE=93343925; PubMed=7688222;
RA Iwase T., Tanaka M., Suzuki M., Naito Y., Sugimura H., Kino I.,
RT "Identification of protein-tyrosine kinase genes preferentially
RT expressed in embryo stomach and gastric cancer.";
RL Biochem. Biophys. Res. Commun. 194:698-705(1993).
[3]
RN SEQUENCE FROM N.A. (ISOFORM LONG).
RP TISSUE=Fetal brain;
RC TISSUE=Fetal brain;
RX MEDLINE=98359217; PubMed=9696046;
RA Tang X.X., Pleasure D.B., Brodeur G.M., Ikegaki N.,
RT "A variant transcript encoding an isoform of the human protein
RT tyrosine kinase EPHB2 is generated by alternative splicing and
RT alternative use of polyadenylation signals.";
RL Oncogene 17:521-526(1998).
[4]
RN SEQUENCE OF 15-986 FROM N.A. (ISOFORM SHORT).
RP TISSUE=Brain;
RC TISSUE=Brain;
RX MEDLINE=95206782; PubMed=7898931;
RA Fox G.M., Holst P.L., Chute H.T., Lindberg R.A., Janssen A.M.,
RA Basu R., Welcher A.A.,
RT "cDNA cloning and tissue distribution of five human EPH-like receptor
RT protein-tyrosine kinases.";
RL Oncogene 10:897-905(1995).
[5]
RN SEQUENCE OF 509-986 FROM N.A. (ISOFORM SHORT).
RP TISSUE=Brain;
RC TISSUE=Brain;
RA Saito T., Naohiko S., Kitahara M., Murata M., Yamamoto Y.,
RA Hori T., Matsuda Y.,
RL Submitted (Aug-1994) to the EMBL/GenBank/DBJ databases.
[6]
RN SEQUENCE OF 652-712 FROM N.A.
RP MEDLINE=91296384; PubMed=1648701;
RA Chan J., Watt V.M.,
RT "week and erk, new members of the eph subclass of receptor protein-
RT tyrosine kinases.";
RL Oncogene 6:1057-1061(1991).
[7]
RN X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) OF 910-986 (ISOFORM SHORT).
RP MEDLINE=99132419; PubMed=9933164;
RX Thamos C.D., Goodwill K.E., Bowie J.U.,
RA "Oligomeric structure of the human EphB2 receptor SAM domain.";
RL Science 283:833-836(1999).
CC -1- FUNCTION: Receptor for members of the ephrin-B family.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBUNIT: The ligand-activated form interacts with multiple
CC proteins, including Grb2-activating protein (RASGAP) through its
CC SH2 domain. Binds RASGAP through the juxtamembrane tyrosines
CC residues. Interacts with PRKCBP (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long; Synonyms=EPHB2V;
CC IsoId=P29323-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=P29323-2; Sequence=VSP_003016, VSP_003017;
CC -1- TISSUE SPECIFICITY: Brain, heart, lung, kidney, placenta,
CC pancreas, liver and skeletal muscle. Preferentially expressed in
CC fetal brain.
CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin
CC receptor subfamily.

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CC -----
 DR EMBL; L41939; AAA99310.1; -
 DR EMBL; D31661; BAA0506.1; -
 DR EMBL; AF025304; AAB84602.1; -
 DR EMBL; D14717; BAA03537.1; -
 DR EMBL; L36643; AAA74244.1; -
 DR EMBL; D37827; BAA07073.1; -
 DR EMBL; X59292; CAA41981.1; -
 DR PIR; A57174; A57174.
 DR PDB; 1BAF; 16-FEB-99.
 DR PDB; 1F0W; 04-JUL-00.
 DR Genew; HXNC3393; EPHB2.
 DR MIM; 600997; -
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0005005; F:transmembrane-ephrin receptor activity; TAS.
 DR GO; GO:0007399; P:neurogenesis; TAS.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
 DR InterPro; IPR006209; EGF-like
 DR InterPro; IPR001090; Ephrin_receptor.
 DR InterPro; IPR008957; FN-III-like.
 DR InterPro; IPR003961; FN-III.
 DR InterPro; IPR003962; FNIII subd.
 DR InterPro; IPR008979; Gal bind like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001660; SAM.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR InterPro; IPR01426; YKase_receptor.
 DR Pfam; PF00041; fn3_2.
 DR Pfam; PF00069; PKinase; 1.
 DR Pfam; PF00536; SAM; 1.
 DR PRINTS; PR00014; FNTPRIT.
 DR PRINTS; PR00109; TyRKINASE.
 DR ProDom; PD001495; Ephrin_receptor; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00615; Eph_lbd; 1.
 DR SMART; SM00060; FN3_2.
 DR SMART; SM00454; SAM; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE; PS00790; RECEPTOR TYR KIN V_1; 1.
 DR PROSITE; PS00791; RECEPTOR TYR KIN V_2; 1.
 DR PROSITE; PS0105; SAM DOMAIN; 1.
 DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal; 3d-structure;
 KW Alternative splicing; Repeat.
 FT SIGNAL 1 18
 FT CHAIN 19 1055
 FT DOMAIN 19 543
 FT TRANSMEM 544 564
 FT DOMAIN 565 1055
 FT DOMAIN 184 324
 FT DOMAIN 325 418
 FT DOMAIN 436 520
 FT DOMAIN 621 884
 FT SITE 913 977
 FT SITE 984 986
 FT NE_BIND 627 635
 FT BINDING 653 653
 FT ACT SITE 746 746
 FT MOD_RES 596 596
 FT MOD_RES 602 602
 FT MOD_RES 780 780
 FT MOD_RES 930 930
 FT MOD_RES 930 930
 FT CARBOHYD 265 265
 FT CARBOHYD 336 336
 FT CARBOHYD 428 428
 FT CARBOHYD 482 482

FT VARSPPLIC 986 986 G -> V (in isoform Short).
 FT VARSPPLIC 987 1055 Missing (in isoform Short).
 FT VARSPPLIC 987 1055 Missing (in isoform Short).
 FT VARIANT 671 671 A -> R.
 FT CONFLICT 1 20 /ftid=VAR_004162.
 FT CONFLICT 1 20 MALRRLGALLLLPLLAAVEETLMDSTTATATAGLGMVHPSPSGMEVSGYDENMNTIRTYQ
 FT CONFLICT 154 154 G -> D (IN REF. 2).
 FT CONFLICT 476 476 K -> KO (IN REF. 2).
 FT CONFLICT 495 496 MISSING (IN REF. 4).
 FT CONFLICT 532 532 E -> D (IN REF. 2).
 FT CONFLICT 568 568 R -> RR (IN REF. 1).
 FT CONFLICT 589 589 M -> I (IN REF. 4).
 FT CONFLICT 788 788 I -> F (IN REF. 4).
 FT CONFLICT 853 853 S -> A (IN REF. 2 AND 5).
 FT CONFLICT 923 923 E -> K (IN REF. 2 AND 5).
 FT CONFLICT 956 956 L -> V (IN REF. 3).
 FT CONFLICT 958 958 V -> L (IN REF. 1).
 FT HELIX 918 924
 FT HELIX 925 926
 FT HELIX 928 930
 FT HELIX 931 936
 FT TURN 937 938
 FT HELIX 942 945
 FT TURN 946 947
 FT HELIX 950 956
 FT TURN 957 957
 FT HELIX 961 984
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 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1054; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MALRRLGALLLLPLLAAVEETLMDSTTATATAGLGMVHPSPSGMEVSGYDENMNTIRTYQ 60
 DB 1 MALRRLGALLLLPLLAAVEETLMDSTTATATAGLGMVHPSPSGMEVSGYDENMNTIRTYQ 60
 QY 61 VCNVPESSQNNWLFRTKTRRRGARHIVEMKFSYRDCSSIPSPGCKETFNLYYEADF 120
 DB 61 VCNVPESSQNNWLFRTKTRRRGARHIVEMKFSYRDCSSIPSPGCKETFNLYYEADF 120
 QY 61 VCNVPESSQNNWLFRTKTRRRGARHIVEMKFSYRDCSSIPSPGCKETFNLYYEADF 120
 DB 61 VCNVPESSQNNWLFRTKTRRRGARHIVEMKFSYRDCSSIPSPGCKETFNLYYEADF 120
 QY 121 DSAIKTPNNMNMENWVVDITIADESFSQVDLGRVWKINTEVRSFPGVRSRSGFYLAFO 180
 DB 121 DSAIKTPNNMNMENWVVDITIADESFSQVDLGRVWKINTEVRSFPGVRSRSGFYLAFO 180
 QY 121 DSAIKTPNNMNMENWVVDITIADESFSQVDLGRVWKINTEVRSFPGVRSRSGFYLAFO 180
 DB 121 DSAIKTPNNMNMENWVVDITIADESFSQVDLGRVWKINTEVRSFPGVRSRSGFYLAFO 180
 QY 181 YGGCMSLIADVVFYKCPRIIIONGAIFQETLGAESTSLVAARGSCIANAEVDVPIKLY 240
 DB 181 YGGCMSLIADVVFYKCPRIIIONGAIFQETLGAESTSLVAARGSCIANAEVDVPIKLY 240
 QY 241 CNGGEMLVPIGRGCKAGFEAVENGTVCGCPGCTFKANQSGEACTHCINSRTTSEGA 300
 DB 241 CNGGEMLVPIGRGCKAGFEAVENGTVCGCPGCTFKANQSGEACTHCINSRTTSEGA 300
 QY 241 CNGGEMLVPIGRGCKAGFEAVENGTVCGCPGCTFKANQSGEACTHCINSRTTSEGA 300
 DB 241 CNGGEMLVPIGRGCKAGFEAVENGTVCGCPGCTFKANQSGEACTHCINSRTTSEGA 300
 QY 301 TNCVCRNGYRADLPLDMECTTIPSAPOAVISSVNETSLMLBTPRDSGREDLVYNI 360
 DB 301 TNCVCRNGYRADLPLDMECTTIPSAPOAVISSVNETSLMLBTPRDSGREDLVYNI 360
 QY 301 TNCVCRNGYRADLPLDMECTTIPSAPOAVISSVNETSLMLBTPRDSGREDLVYNI 360
 DB 301 TNCVCRNGYRADLPLDMECTTIPSAPOAVISSVNETSLMLBTPRDSGREDLVYNI 360
 QY 361 ICKCGSGRACRCGNNVQYARQGLTEPRYISDLAHYQYTBIAQVNVGTQSPF 420
 DB 361 ICKCGSGRACRCGNNVQYARQGLTEPRYISDLAHYQYTBIAQVNVGTQSPF 420
 QY 361 ICKCGSGRACRCGNNVQYARQGLTEPRYISDLAHYQYTBIAQVNVGTQSPF 420
 DB 361 ICKCGSGRACRCGNNVQYARQGLTEPRYISDLAHYQYTBIAQVNVGTQSPF 420
 QY 421 SPQASVNTITNQAPAVSIVHQSRTVDSITLSMQPQPGVILDELYQYKELSE 480
 DB 421 SPQASVNTITNQAPAVSIVHQSRTVDSITLSMQPQPGVILDELYQYKELSE 480
 QY 481 YNATAISPTNYTVVQGLKAGIYVQVRAETVAGIGRISGKNYFQTMBAEYQTSIQEK 540
 DB 481 YNATAISPTNYTVVQGLKAGIYVQVRAETVAGIGRISGKNYFQTMBAEYQTSIQEK 540
 QY 541 LPLTIGSSAGLVFLAVVVAIVCNRRGERADSEYTDPLQYTGSHMTPGMKIYIDPF 600
 DB 541 LPLTIGSSAGLVFLAVVVAIVCNRRGERADSEYTDPLQYTGSHMTPGMKIYIDPF 600

Db 541 LPLIGSSAAGVLLAVVIAIVCNRRGERADSEYTDKLOHYTSGHMTGNKXIYDF 600
 QY 601 TYEDPNAVEEFAKEIDISCVKIEQVIGAGEFGEVSCGHLKPKREIFAIXTLKSGYT 660
 Db 601 TYEDPNAVEEFAKEIDISCVKIEQVIGAGEFGEVSCGHLKPKREIFAIXTLKSGYT 660
 QY 661 EKGRDPLSASIMGQFDHPNVTHLSGVTKSTPVMITTEFMENGSLDSFLRNDQOFTV 720
 Db 661 EKGRDPLSASIMGQFDHPNVTHLSGVTKSTPVMITTEFMENGSLDSFLRNDQOFTV 720
 QY 721 IOLVGMRLGTAAMKTYADNKNVYHRDLAARNILVNSLVCKVSDPGLSRPLEDDTSDPY 780
 Db 721 IOLVGMRLGTAAMKTYADNKNVYHRDLAARNILVNSLVCKVSDPGLSRPLEDDTSDPY 780
 QY 781 TSAAGKIPIRMTAPEAIOYRKFTSASDVMSYGIVMWEVMSYGERPYMDTNDVINAIE 840
 Db 781 TSAAGKIPIRMTAPEAIOYRKFTSASDVMSYGIVMWEVMSYGERPYMDTNDVINAIE 840
 QY 841 QDRLPPEMPCPSALHQLMDCKQKDNHRPKFGQIVNTLDKXIRPNLSIKAAPISSGI 900
 Db 841 QDRLPPEMPCPSALHQLMDCKQKDNHRPKFGQIVNTLDKXIRPNLSIKAAPISSGI 900
 QY 901 NLPLDRTIPDYTSFNTVDEMLAIXMGQYKESFANAGFTSPDVMSQMMEDILRVGTVL 960
 Db 901 NLPLDRTIPDYTSFNTVDEMLAIXMGQYKESFANAGFTSPDVMSQMMEDILRVGTVL 960
 QY 961 AGHOKKILINSIQWRAQMNQIQSEVQGLAPRRPARGTRKRCOPRVYKTCNSNDGKK 1020
 Db 961 AGHOKKILINSIQWRAQMNQIQSEVQGLAPRRPARGTRKRCOPRVYKTCNSNDGKK 1020
 QY 1021 GMSGKKTDPGRGREIOGIFPKESHKESNDSCSG 1055
 Db 1021 GMSGKKTDPGRGREIOGIFPKESHKESNDSCSG 1055

RESULT 2
 EPR2_MOUSE STANDARD: PRT; 994 AA.
 ID EPR2_MOUSE STANDARD: PRT; 994 AA.
 AC P54763: 062213: Q9QVY4:
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Ephrin type-B receptor 2 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor Eph-3) (Neural kinase) (Nuk receptor tyrosine kinase) (SEK-3).
 GN EPHB2 OR EPH3 OR NUK OR SEK3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94181250; PubMed=8134103;
 RA Henkemeyer M., Melengere L.E., McGlade J., Olivier J.P., Conlon R.A., Holmward D.P., Letwin K., Pawson T.;
 RT "Immunolocalization of the Nuk receptor tyrosine kinase suggests roles in segmental patterning of the brain and axonogenesis";
 RL Oncogene 9:1001-1014(1994).
 RN [2]
 RP SEQUENCE OF 516-994 FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Brain;
 RX MEDLINE=95034306; PubMed=7947319;
 RA Becker N., Seltanidou T., Murphy P., Mattei M.-G., Topilko P., Nieto A., Wilkinson D.G., Charney P., Gilardi P.;
 RT "Several receptor tyrosine kinase genes of the Eph family are segmentally expressed in the developing hindbrain";
 RL Mech. Dev. 47:3-17(1994).
 RN [3]
 RP FUNCTION
 RX MEDLINE=20171264; PubMed=10704386;
 RA Mondal R., Wideman C., Kaprielian Z.;
 RT "Complementary expression of transmembrane ephrins and their receptors in the mouse spinal cord: a possible role in constraining the

RT orientation of longitudinally projecting axons.";
 RL Development 127:1397-1410(2000).
 RN [4]
 RP INTERACTION WITH PRKCABP.
 RX MEDLINE=99098206; PubMed=9883737;
 RA Torres R., Firestein B.U., Dong H., Staudinger J., Olson E.N., Huganir R.L., Bredt D.S., Gale N.W., Yancopoulos G.D.;
 RT "PDZ proteins bind, cluster, and synaptically colocalize with Eph receptors and their ephrin ligands";
 RL Neuron 21:1453-1463(1998).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 29-204.
 RX MEDLINE=99068648; PubMed=9853759;
 RA Himanen J.-P., Henkemeyer M., Nikolov D.B.;
 RT "Crystal structure of the ligand-binding domain of the receptor tyrosine kinase EphA2";
 RL Nature 396:486-491(1998).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 29-208 IN COMPLEX WITH EPHRIN-B2.
 RX MEDLINE=21639766; PubMed=11780069;
 RA Himanen J.-P., Rajashankar K.R., Lackmann M., Cowan C.A., Henkemeyer M., Nikolov D.B.;
 RT "Crystal structure of an Eph receptor-ephrin complex";
 RL Nature 414:933-938(2001).
 CC - FUNCTION: Receptor for members of the ephrin-B family. Can function in aspects of retinal ganglion cell axon guidance to the optic disk even lacking its tyrosine kinase domain.
 CC - CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
 CC - SUBUNIT: Interacts with PRKCABP. The ligand-activated form interacts with multiple proteins, including GTPase-activating protein (RASGAP) through its SH2 domain. Binds RASGAP through the juxtamembrane tyrosine residues. Interacts with PRKCABP (by similarity).
 CC - SUBCELLULAR LOCATION: Type I membrane protein.
 CC - TISSUE SPECIFICITY: Expressed in cells of the developing outer retina.
 CC - SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC - SIMILARITY: Contains 2 fibronectin type III domains.
 CC - SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin receptor subfamily.
 CC -----
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 CC -----
 DR EMBL, I25890; AA872411.1; ALT_INIT.
 DR EMBL, X76011; CA853598.1; -.
 DR PDB; 1KGY; 28-MAY-02.
 DR PDB; INUK; 13-OCT-99.
 DR MGD; MGI:99611; Ephb2.
 DR GO; GO:0008046; F:axon guidance receptor activity; IDA.
 DR GO; GO:0007411; P:axon guidance; IDA.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR001090; Ephrin_receptor.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR003962; FNIII_subd.
 DR InterPro; IPR008979; Gal_bind-like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001660; SAM.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR InterPro; IPR001426; YKase_receptorV.
 DR Pfam; PF01404; Eph_1bd; 1.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00069; kinase; 1.
 DR Pfam; PF00536; SAM; 1.

DR PRINTS; PRO0014; FNTYPEIII.
 DR PRINTS; PRO0109; TYRKINASE.
 DR Prodom; PD001495; Ephrin_receptor; 1.
 DR Prodom; PD000001; Prot_kinase; 1.
 DR SMART; SM000615; Eph_Lbd; 1.
 DR SMART; SM000600; FN3; 2.
 DR SMART; SM00454; SAM; 1.
 DR SMART; SM00219; TykC; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN 1.
 DR PROSITE; PS01107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS0105; SAM DOMAIN; 1.
 DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat; 3d-structure.
 FT SIGNAL 1 26
 FT CHAIN 1 994
 FT DOMAIN 27 551
 FT TRANSMEM 552 572
 FT DOMAIN 573 994
 FT DOMAIN 192 329
 FT DOMAIN 330 439
 FT DOMAIN 440 537
 FT DOMAIN 629 892
 FT DOMAIN 921 985
 FT SITE 992 994
 FT NP_BIND 635 643
 FT BINDING 661 661
 FT ACT_SITE 754 754
 FT MOD_RES 604 604
 FT MOD_RES 610 610
 FT MOD_RES 788 788
 FT MOD_RES 938 938
 FT DISULFID 70 192
 FT DISULFID 105 115
 FT CARBOHYD 273 273
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 FT CONFLICT 576 576
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Query Match 92.1%; Score 5129; DB 1; Length 994;
 Best Local Similarity 99.6%; Pred. No. 1.2e-314;
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QY 10 LLLPLLAAYEETLMDSTATAELGAWVHPDPSGMEVSGYDENMNTIRIYQVCNVESSQ 69
 DB 18 LLLPLLAAYEETLMDSTATAELGAWVHPDPSGMEVSGYDENMNTIRIYQVCNVESSQ 77
 QY 70 NNMIRTFFIRRGARHIVHEMKFSYRDCSIPSPVPGCKETPNLYYEADFDLAKTTPN 129
 DB 78 NNMIRTFFIRRGARHIVHEMKFSYRDCSIPSPVPGCKETPNLYYEADFDLAKTTPN 137
 QY 130 WMENPWKVDITIADESFQVDLGRVYKINTEVRSFGVRSGLFYLAFOQYGCMSLIA 189
 DB 138 WMENPWKVDITIADESFQVDLGRVYKINTEVRSFGVRSGLFYLAFOQYGCMSLIA 197
 QY 190 VRVYRKCPRIIONGAFQETLSGASTSLVAARGSCIANAEVDVPILKYCNGDEBVL 249
 DB 198 VRVYRKCPRIIONGAFQETLSGASTSLVAARGSCIANAEVDVPILKYCNGDEBVL 257
 QY 250 PIGCMCKAGBEAVENTGVRGCPGTFKANOGEACTHCPINSRTSSEGTATCYCRNGY 309
 DB 258 PIGCMCKAGBEAVENTGVRGCPGTFKANOGEACTHCPINSRTSSEGTATCYCRNGY 317
 QY 310 YRADLDLPDMPCTTIPSAPOAVISVNETSLMLWTPPRDSGREDLVNIIKSCGSGR 369
 DB 318 YRADLDLPDMPCTTIPSAPOAVISVNETSLMLWTPPRDSGREDLVNIIKSCGSGR 377
 QY 370 GACTRCGDNVYARQGLTEPRYISDLAHTQYTFEIQAVNGVTDQSPFSPQFASVNI 429

DB 378 GACTRCGDNVYARQGLTEPRYISDLAHTQYTFEIQAVNGVTDQSPFSPQFASVNI 437
 QY 430 TTNQAAPSAVSIMQOVARTVDSITLSWSOPQPGVILDELOYEKELESEYNATAIKSP 489
 DB 438 TTNQAAPSAVSIMQOVARTVDSITLSWSOPQPGVILDELOYEKELESEYNATAIKSP 497
 QY 490 TTNVVOGLKAGAIYVQVARTVAGYGRYSGKMYFQTMTEAEYQTSIOEKLPIIGSSA 549
 DB 498 TTNVVOGLKAGAIYVQVARTVAGYGRYSGKMYFQTMTEAEYQTSIOEKLPIIGSSA 557
 QY 550 AGVFLVAVVIAVVCNRRGFEERADSEYTKLQHYTSGHMTPGKIIYIDPFTYCDPNAV 609
 DB 558 AGVFLVAVVIAVVCNRRGFEERADSEYTKLQHYTSGHMTPGKIIYIDPFTYCDPNAV 617
 QY 610 REFAKEIDISCVKIEQVIGAGEFGEVCSGHILKPGKEIFVAIKTLKSGYTEKQRDFLS 669
 DB 618 REFAKEIDISCVKIEQVIGAGEFGEVCSGHILKPGKEIFVAIKTLKSGYTEKQRDFLS 677
 QY 670 EASIMGQDHNRYVHLEGVYTKSTFPWMIITEFMENGLSDSFLRNDQGFYIQVGMRLG 729
 DB 678 EASIMGQDHNRYVHLEGVYTKSTFPWMIITEFMENGLSDSFLRNDQGFYIQVGMRLG 737
 QY 730 IAAGMKYADANVYHRDLAARNILVNSNLVCKVSDFLSFLBDDTSDDPTYSALGKIP 789
 DB 738 IAAGMKYADANVYHRDLAARNILVNSNLVCKVSDFLSFLBDDTSDDPTYSALGKIP 797
 QY 790 IRMTAPEAIQYRKTSASDVWSYGIVMVEVNSYGERPYWMTNODVINAIEQYRLPEPM 849
 DB 798 IRMTAPEAIQYRKTSASDVWSYGIVMVEVNSYGERPYWMTNODVINAIEQYRLPEPM 857
 QY 850 DCPGSLHQLMDCKQKRNHRPKFGQIVNTLDKMIIRPNLSIKAPAPLSSGINLPILDRTI 909
 DB 858 DCPGSLHQLMDCKQKRNHRPKFGQIVNTLDKMIIRPNLSIKAPAPLSSGINLPILDRTI 917
 QY 910 PDYTSFNTVDEMLAIKMGQYKESFANAGFTSPDVVSQMMMEDILRVGVTLAHOXKILN 969
 DB 918 PDYTSFNTVDEMLAIKMGQYKESFANAGFTSPDVVSQMMMEDILRVGVTLAHOXKILN 977
 QY 970 SIQVRAQMOIQSVE 985
 DB 978 SIQVRAQMOIQSVE 993

Search completed: August 28, 2004, 04:09:27
 Job time : 20.6423 secs

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OM protein - protein search, using sw model

Run on: August 28, 2004, 04:02:25 ; Search time 34.1156 Seconds

(without alignments)
2974.650 Million cell updates/sec

Title: US-09-914-883-4

Perfect score: 5571
Sequence: 1 MALRLGAAALLPLLAAYE.....QGIFKEDSHKESNDCSCG 1055Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 90%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR:78:*
2: PIR:2:*
3: PIR:3:*
4: PIR:4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	5088	91.3	970	2 178842	receptor protein-t

ALIGNMENTS

RESULT 1
178842
receptor protein-tyrosine kinase - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 29-May-1998 #sequence_revision 29-May-1998 #ext_change 18-Jun-1999
C/Accession: 178842

R/Ref: G.M.; Holte, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu, R.; Weicher,
Oncogene 10, 897-905, 1995
A/Title: cDNA cloning and tissue distribution of five human Eph-like receptor protein-ty
A/Reference number: T58351, MIMD:95206782, PMID:7898931

A/Accession: 178842
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-970 <RES>

A/Cross-references: GB:U36643; NID:G551609; PIDN:AAV4244.1; PID:G551610
A/Genes: HKX5
C/Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
F:603-871/Domain: protein kinase homology <KIN>
F:894-960/Domain: SAM homology <SAM>

Query Match 91.3%; Score 5088; DB 2; Length 970;
Best Local Similarity 99.5%; Pred. No. 1.2e-231;

Matches 966; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY	15	LLAAVEETLMSTTATLAWVHPSPGMEVSGVDENNTIRTVQVNVPESSQNNMLR	74
DB	1	LLAAVEETLMSTTATLAWVHPSPGMEVSGVDENNTIRTVQVNVPESSQNNMLR	60
QY	75	TKFIRRGARHRIHVMKESVSDCSIPSPGCKETFNLYYYEADFDSATKTFPMWENP	134
DB	61	TKFIRRGARHRIHVMKESVSDCSIPSPGCKETFNLYYYEADFDSATKTFPMWENP	120
QY	135	WKVDTTIADESFSQVDIGRVMKINTVRSFGPVSRSRGFTLAFQDYGCCSLAVRPFY	194
DB	121	WKVDTTIADESFSQVDIGRVMKINTVRSFGPVSRSRGFTLAFQDYGCCSLAVRPFY	180
QY	195	RKCPRIIONGAIPOETLSGAESTSLVAARGSCIANAEVDVPIKLYCGDGEMLVPIGRG	254
DB	181	RKCPRIIONGAIPOETLSGAESTSLVAARGSCIANAEVDVPIKLYCGDGEMLVPIGRG	240
QY	255	MCKAGFEAVENGTVCRGPGSGTFKANOQDEACTHCPINSRTTBGATNCVCRNGYRADL	314
DB	241	MCKAGFEAVENGTVCRGPGSGTFKANOQDEACTHCPINSRTTBGATNCVCRNGYRADL	300
QY	315	DLDMPCCTTIPSAPOAVISSVNETSLMELMTPPRDSGREDLVNIIICKSGSGRGACTR	374
DB	301	DLDMPCCTTIPSAPOAVISSVNETSLMELMTPPRDSGREDLVNIIICKSGSGRGACTR	360
QY	375	CGDNVQYAPROLGLTEPRITYSLLAHQYTFEEIQAVNVGTDQSPFSPQFASVNTTNOA	434
DB	361	CGDNVQYAPROLGLTEPRITYSLLAHQYTFEEIQAVNVGTDQSPFSPQFASVNTTNOA	420
QY	435	APSAVSIHQVSRVTDSTLMSQDPQNGVILDYELQYEREKELSEYNATAIKSTNTVT	494
DB	421	APSAVSIHQVSRVTDSTLMSQDPQNGVILDYELQYEREKELSEYNATAIKSTNTVT	480
QY	495	VOGLKAGAIYFQVARTVAGYGRSGRMVFOITAEYQTSIOEKLPLIGSSAGLVF	554
DB	481	--GLKAGAIYFQVARTVAGYGRSGRMVFOITAEYQTSIOEKLPLIGSSAGLVF	538
QY	555	LIAVVVIAIVCNRRGFEPADESYTDKLOHYTSGHMTPEMKIYIDPFYEDPNEAVEBP	614
DB	539	LIAVVVIAIVCNRRGFEPADESYTDKLOHYTSGHMTPEMKIYIDPFYEDPNEAVEBP	598
QY	615	EIDISCVAIEQVIGAFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORBDPSEASIM	674
DB	599	EIDISCVAIEQVIGAFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORBDPSEASIM	658
QY	675	GQFDHPNVIHLEGVVTKSTPVMIIITFPMENGSLDSFLRQNDGQFTVIQVGLRGIAAGM	734
DB	659	GQFDHPNVIHLEGVVTKSTPVMIIITFPMENGSLDSFLRQNDGQFTVIQVGLRGIAAGM	718
QY	735	KYLADNMYVHRDLAARNILVNSLVCKVSDRGLSRFLEDPDTPSYTALGKPIRPTA	794
DB	719	KYLADNMYVHRDLAARNILVNSLVCKVSDRGLSRFLEDPDTPSYTALGKPIRPTA	778
QY	795	PEALQYRKFTSASDVSYGIVMWEVMSYGERPYDMTNOQVINAIEQDYRLPPEWDCPSA	854
DB	779	PEALQYRKFTSASDVSYGIVMWEVMSYGERPYDMTNOQVINAIEQDYRLPPEWDCPSA	838
QY	855	LHQLMLDQWQDRNHRPFEGQIVNTLDMKINPNPSLAKMAALSGSINPLDRTTIPDTS	914
DB	839	LHQLMLDQWQDRNHRPFEGQIVNTLDMKINPNPSLAKMAALSGSINPLDRTTIPDTS	898
QY	915	FNTVDWELEAIKMGQYKESFANAGFTSPDVVSQMMWEDILVGTVTLGHQKKIINSICVM	974
DB	899	FNTVDWELEAIKMGQYKESFANAGFTSPDVVSQMMWEDILVGTVTLGHQKKIINSICVM	958
QY	975	RAQXNQIOISVE 985	
DB	959	RAQXNQIOISVE 969	

Search completed: August 28, 2004, 04:14:05
Job time : 35.1156 secs

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: August 28, 2004, 04:00:54 ; Search time 103.898 Seconds

(without alignments)
3203.844 Million cell updates/sec

Title: US-09-914-883-4

Perfect score: 5571

Sequence: 1 MAIRRGALLLLPLLAAYE.....QGIFKEDSKESNDSCGG 1055

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 90%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SP archaea:*
- 2: SP bacteria:*
- 3: SP fungi:*
- 4: SP human:*
- 5: SP invertebrate:*
- 6: SP mammal:*
- 7: SP mhc:*
- 8: SP organelle:*
- 9: SP phage:*
- 10: SP plant:*
- 11: SP rodent:*
- 12: SP virus:*
- 13: SP vertebrate:*
- 14: SP unclassified:*
- 15: SP viirus:*
- 16: SP bacteriaph:*
- 17: SP archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5129	92.1	994	11 Q9QVY4	Q9qvy4 mus sp. neu

ALIGNMENTS

RESULT 1
Q9QVY4
ID Q9QVY4
AC Q9QVY4
DT 01-MAY-2000 (TRENBLREL 13, Created)
DT 01-OCT-2003 (TRENBLREL 25, Last annotation update)
DE Neutral kinase, NUK-EPH/ELK/ECK family tyrosine kinase (EC 2.7.1.115) (Ephrin receptor) (Tyrosine-protein kinase receptor).
PRELIMINARY; PRT; 994 AA.

OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94181250; PubMed=8134103;
RA Henkemeyer M., Margengler J.E., McGlade J., Olivier J.P., Conlon R.A.,
RA Holyard D.P., Letwin K., Pawson T.,
RT "Immunolocalization of the Nuk receptor tyrosine kinase suggests roles
RT in segmental patterning of the brain and axonogenesis.";
RL Oncogene 9:1001-1014(1994).
CC -I- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
CC TYROSINE PHOSPHATE
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
CC RECEPTOR SUBFAMILY.
CC HSP; P29323; IBAF.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005524; F: ATP binding; IEA.
DR GO: GO:0005003; F: ephrin receptor activity; IEA.
DR GO: GO:0004713; F: protein-tyrosine kinase activity; IEA.
DR GO: GO:0004872; F: receptor activity; IEA.
DR GO: GO:0016740; F: transferase activity; IEA.
DR GO: GO:0006468; P: protein amino acid phosphorylation; IEA.
DR GO: GO:0007169; P: transmembrane receptor protein tyrosine kin. .; IEA.
DR InterPro: IPR006309; EGF like.
DR InterPro: IPR001090; Ephrin_receptor.
DR InterPro: IPR003962; FNIII_stud.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR008979; Gal_bind_like.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR001660; SAM.
DR InterPro: IPR001245; Tyr_kinase.
DR InterPro: IPR008266; Tyr_kinase_AS.
DR InterPro: IPR001426; Ykase_receptorIV.
DR Pfam: PF01404; EPH_Lbd; 1.
DR Pfam: PF00041; fn3; 2.
DR Pfam: PF00069; kinase; 1.
DR Pfam: PF00536; SAM; 1.
DR PRINTS: PRO0014; FNTYPRIT.
DR PRINTS: PRO0109; TYRKINASE.
DR ProDom: PD001495; Ephrin_receptor; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00615; EPH_Lbd; 1.
DR SMART: SM00060; FN3; 2.
DR SMART: SM00454; SAM; 1.
DR SMART: SM00219; TyKc; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS0107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE: PS0105; SAM_DOMAIN; 1.
KW ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor; Repeat;
KW Transference; Transmembrane; Tyrosine-protein kinase.
SQ SEQUENCE 994 AA; 110759 MW; ECGB9B12A070394C CRC64;
Query Match 92.1%; Score 5129; DB 11; Length 994;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 972; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 10 LLLPLLAAYEETLNDSTTATLGLGMVHPSPGMEVSGYDENNTIFRTYQVCNVFESSQ 69
DB 18 LLLPLLAAYEETLNDSTTATLGLGMVHPSPGMEVSGYDENNTIFRTYQVCNVFESSQ 77
QY 70 NNMILTKTFRRGARIVHEKFSYVDCSSIPSYGSCKEFNLYYADPFSATKTPN 129
DB 78 NNMILTKTFRRGARIVHEKFSYVDCSSIPSYGSCKEFNLYYADPFSATKTPN 137
QY 130 WMENPVMKVDITADESFSQVDLGRVWKINTEVASFGVSRSGFYLAFODYGGCMSLIA 189

Db	138	WMENPWKVDITIADESFSDVLDGRMKNTFVRSGFVSRNGFYIAFDYGGCKSLIA	197
Qy	190	VRVYRKCPRIIIONGAIFQETLSGAESTSLVAPRGSCIANAEYDVPIKLYCNGDGEWLY	249
Db	198	VRVYRKCPRIIIONGAIFQETLSGAESTSLVAPRGSCIANAEYDVPIKLYCNGDGEWLY	257
Qy	250	PIGRCKAGFEAVENGTVCRGCPSTFKANOGDEACTHCPINSRTSSECATNCVRNGY	309
Db	258	PIGRCKAGFEAVENGTVCRGCPSTFKANOGDEACTHCPINSRTSSECATNCVRNGY	317
Qy	310	YRADLDPLDMFCCTIPAPQAVISSVNETSLMELWTPPRDGGREDLVYNIICKSCGSGR	369
Db	318	YRADLDPLDMFCCTIPAPQAVISSVNETSLMELWTPPRDGGREDLVYNIICKSCGSGR	377
Qy	370	GACTRCGDNOYARROGLTEPRYISDILAHQYTFEIQAVNGVTDOSPSPQFASVNI	429
Db	378	GACTRCGDNOYARROGLTEPRYISDILAHQYTFEIQAVNGVTDOSPSPQFASVNI	437
Qy	430	TTNOAPSAYSIMHQSRTVDSITLSWSQDPQNGVILDELYEYKEKESEYNATAIKSP	489
Db	438	TTNOAPSAYSIMHQSRTVDSITLSWSQDPQNGVILDELYEYKEKESEYNATAIKSP	497
Qy	490	TNTVTGGLGAGAIYVQVARTAGYGRYSCKMYFOTMTEAEYQTSIOEKLPLIIGSSA	549
Db	498	TNTVTGGLGAGAIYVQVARTAGYGRYSCKMYFOTMTEAEYQTSIOEKLPLIIGSSA	557
Qy	550	AGLVFLIAVVVIAIVCNRGFERADSEYTDLOHTSGHMTPGMKIYIDPFTEYEDPNEAV	609
Db	558	AGLVFLIAVVVIAIVCNRGFERADSEYTDLOHTSGHMTPGMKIYIDPFTEYEDPNEAV	617
Qy	610	REFAKEIDISGVKEQYIGAGEPEVCSGHLKLPKREIFVAIKTLKSGYTEKORDFLS	669
Db	618	REFAKEIDISGVKEQYIGAGEPEVCSGHLKLPKREIFVAIKTLKSGYTEKORDFLS	677
Qy	670	EASIMQFDPHNVHLEGVVTKSTPVMITEFMENGSLSDFLRONDQFTVIQVGMIRG	729
Db	678	EASIMQFDPHNVHLEGVVTKSTPVMITEFMENGSLSDFLRONDQFTVIQVGMIRG	737
Qy	730	IAAGMKTLADMYVHRDLAARNILVNSLVCKVSDFGLSRFLDDTSDPTYSALGKIP	789
Db	738	IAAGMKTLADMYVHRDLAARNILVNSLVCKVSDFGLSRFLDDTSDPTYSALGKIP	797
Qy	790	IRMTAPALIOYRKFTSASDVMSYGIWMEVMSYGERPYMDTNOYINAEODYRLPPPM	849
Db	798	IRMTAPALIOYRKFTSASDVMSYGIWMEVMSYGERPYMDTNOYINAEODYRLPPPM	857
Qy	850	DGFSALHQLMDCWQKDRNHRPKFGQIVNTLDKXMINRPNLSLKAMAPLSSGILPLDRTI	909
Db	858	DGFSALHQLMDCWQKDRNHRPKFGQIVNTLDKXMINRPNLSLKAMAPLSSGILPLDRTI	917
Qy	910	PDYTSFNTVDEWLEALIMGQYKESFANAGFTSPDVVSQMMEDILRVGVTLAGHOKKILN	969
Db	918	PDYTSFNTVDEWLEALIMGQYKESFANAGFTSPDVVSQMMEDILRVGVTLAGHOKKILN	977
Qy	970	SIQVYRAQNNQIOSVE 985	
Db	978	SIQVYRAQNNQIOSVE 993	

Search completed: August 28, 2004, 04:12:52
 Job time : 103.898 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2004, 03:50:04 ; Search time 104.415 Seconds
(without alignments)
2854.849 Million cell updates/sec

Title: US-09-914-883-4
Perfect score: 5571
Sequence: 1 MALRRLGALLLLPLLAAYE.....QGIFPKDSKESNDSCGCG 1055

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 7

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 90%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Genesegp29Jan04:*
2: genesegp1980s:*
3: genesegp1990s:*
4: genesegp2000s:*
5: genesegp2001s:*
6: genesegp2002s:*
7: genesegp2003as:*
8: genesegp2003bs:*
9: genesegp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5571	100.0	1055	3 AAB19591	Aab19591 Human CAS
2	5571	100.0	1055	6 AB007847	Abu07847 Human eph
3	5170.5	92.8	987	3 AAB19590	Aab19590 Human CAS
4	5129	92.1	994	2 AA026366	Aa026366 Mouse Nuk
5	5129	92.1	994	4 AA01907	Aa01907 Murine ne
6	5125	92.0	994	2 AAR87018	Aar87018 Receptor
7	5092	91.4	970	2 AAR85089	Aar85089 EPH-like

ALIGNMENTS

RESULT 1
ID AAB19591 standard; protein; 1055 AA.

XX AAB19591;

DT 22-JAN-2001 (first entry)

DE Human CASB616.

KW CASB616; EPHB2; ERK; EPH3; EPH3; DRT; HEK5; EPHB2V;

KM receptor protein tyrosine kinase; human; antigen; colon cancer; ovary cancer; autoimmune disease; vaccine; therapy; diagnosis.

XX OS Homo sapiens.
XX PN WO200053216-A2.
XX PD 14-SEP-2000.
XX PF 28-FEB-2000; 2000MO-EP001587.
XX PR 05-MAR-1999; 99GB-00005124.
XX PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX PI Vinals Y De Basolac;
XX DR WPI; 2000-587384/55.
XX DR N-PSDB; AAA88549.
XX PT Vaccine composition for treating ovarian and colon cancer, comprises
XX PT CASB616 polypeptides, polynucleotides or antigen presenting cells
XX PT expressing the polypeptides.
XX PS Claim 1; Page 42; 57pp; English.
XX SS The present sequence is that of human CASB616, a member of the EPH and
XX CC EPH-related family of receptor protein tyrosine kinases. CASB616 is also
XX CC known as EPHB2, ERK, EPH3, EPH3, DRT, HEK5 and EPHB2V. CASB616
XX CC polypeptides and polynucleotides are important immunogens for specific
XX CC prophylactic or therapeutic immunization against tumours, especially
XX CC colon cancer (claimed) and ovarian cancer. They are specifically
XX CC expressed or highly over-expressed in tumours compared to normal cells
XX CC and can thus be targeted by antigen-specific immune mechanisms leading to
XX CC destruction of the tumour cells. They can also be used to diagnose the
XX CC occurrence of tumour cells. Their inappropriate expression can also cause
XX CC an induction of autoimmune responses, which can be corrected through
XX CC vaccination using the CASB616 polypeptides or polynucleotides
SQ Sequence 1055 AA;

Query Match 100.0%; Score 5571; DB 3; Length 1055;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1055; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRRLGALLLLPLLAAYEETLMDSTTAELGMMVHPSPGMEVSGYDENNTIRTYQ 60
DB 1 MALRRLGALLLLPLLAAYEETLMDSTTAELGMMVHPSPGMEVSGYDENNTIRTYQ 60
QY 1 VCNVFESSQNNWLTETKFLRRGARRIHVEMKFSVRDCSIPSVSGCKETENLYYEADF 120
DB 1 VCNVFESSQNNWLTETKFLRRGARRIHVEMKFSVRDCSIPSVSGCKETENLYYEADF 120
QY 121 DSATKTFEPMNEMENPVKVDITLADESFEQVLDGRVWKINTEVRSFGFVSSGFFLAQOD 180
DB 121 DSATKTFEPMNEMENPVKVDITLADESFEQVLDGRVWKINTEVRSFGFVSSGFFLAQOD 180
QY 121 DSATKTFEPMNEMENPVKVDITLADESFEQVLDGRVWKINTEVRSFGFVSSGFFLAQOD 180
DB 121 DSATKTFEPMNEMENPVKVDITLADESFEQVLDGRVWKINTEVRSFGFVSSGFFLAQOD 180
QY 181 YGGCMSLIAVAVFPRKCRITLQNGAIFQETLSGAEFSTLVAAKSGCTANAEVVPITLY 240
DB 181 YGGCMSLIAVAVFPRKCRITLQNGAIFQETLSGAEFSTLVAAKSGCTANAEVVPITLY 240
QY 241 CNGDGEWLVPFGRGCKGKAFVAVENGTVCRGCPGTFKANGDADACTHCPINSRTTSGA 300
DB 241 CNGDGEWLVPFGRGCKGKAFVAVENGTVCRGCPGTFKANGDADACTHCPINSRTTSGA 300
QY 301 TNCVCRNGYPRADLDPLDMCTTTPSAQAVISSVNEFSLMLWTPPPDSGGRDLYVNI 360
DB 301 TNCVCRNGYPRADLDPLDMCTTTPSAQAVISSVNEFSLMLWTPPPDSGGRDLYVNI 360
QY 361 ICKSCSGRGACTCGDGNVOYAPROLGLTEPRYISDLATQYTFELQANGVTDQSPF 420
DB 361 ICKSCSGRGACTCGDGNVOYAPROLGLTEPRYISDLATQYTFELQANGVTDQSPF 420
QY 421 SPQFASVNTTNOAAPSAVSIMHGVSRVDSITLSWSQPDQPNGVILDELYQYEKELSE 480
DB 421 SPQFASVNTTNOAAPSAVSIMHGVSRVDSITLSWSQPDQPNGVILDELYQYEKELSE 480

Db 421 SPOFASVNTTNOAPAVSIMEQVSRITDSTLSNSQDPQNGVILIDYELQYKEKLE 480
QY 481 YNATAIKSPNTVTVOGLKAGAIYVFOVARATVAGYGRYSGKXYFQMTAEAYQTSIOEK 540
XX 481 YNATAIKSPNTVTVOGLKAGAIYVFOVARATVAGYGRYSGKXYFQMTAEAYQTSIOEK 540
QY 541 LPLIGSSAGVFLIAVNVVIAIVCNRRGFERADSETYDLCQYTSGHMTPGKXIYDPF 600
Db 541 LPLIGSSAGVFLIAVNVVIAIVCNRRGFERADSETYDLCQYTSGHMTPGKXIYDPF 600
QY 601 TYEDPNAVREFAKEIDISCVKIEOVIGAGEFEVSGHKLPGKKEIFVAIKTLKSGYT 660
Db 601 TYEDPNAVREFAKEIDISCVKIEOVIGAGEFEVSGHKLPGKKEIFVAIKTLKSGYT 660
QY 661 EKQRRDLSASIMGQFDHPNVVHLBGVTKSTPVMIIIEFPMNSGLDSFLRQNDQFTV 720
Db 661 EKQRRDLSASIMGQFDHPNVVHLBGVTKSTPVMIIIEFPMNSGLDSFLRQNDQFTV 720
QY 721 IOLVGMRGIAAGKYLADNMYVHRDLAARNILVNSLVCKVSDFGLSRFLDSDTDPY 780
Db 721 IOLVGMRGIAAGKYLADNMYVHRDLAARNILVNSLVCKVSDFGLSRFLDSDTDPY 780
QY 781 TSAIGKIPRTWAPPAIQRKTTASDVWSYGIIVMEVMSYGERPYMDMTNODVINAIE 840
Db 781 TSAIGKIPRTWAPPAIQRKTTASDVWSYGIIVMEVMSYGERPYMDMTNODVINAIE 840
QY 841 QDRLPPMDCPSALHQLMDCKQKDNHRPKFGQIVNTLDKIRRNPSLKAAPSSGI 900
Db 841 QDRLPPMDCPSALHQLMDCKQKDNHRPKFGQIVNTLDKIRRNPSLKAAPSSGI 900
QY 901 NLPLDRTIDPYTSFNTVDEMLAIKMGQYKESFANAGFTSPDVASQMMEDILRQVTL 960
Db 901 NLPLDRTIDPYTSFNTVDEMLAIKMGQYKESFANAGFTSPDVASQMMEDILRQVTL 960
QY 961 AGHOKILINSIOWMRAQMNQIOSVEGQPLARRPRAGRTKRCOPRVTKTCSNSDGGKK 1020
Db 961 AGHOKILINSIOWMRAQMNQIOSVEGQPLARRPRAGRTKRCOPRVTKTCSNSDGGKK 1020
QY 1021 GMGKKTDPGRGREIQGIFPKEDSHKESNDSCSG 1055
Db 1021 GMGKKTDPGRGREIQGIFPKEDSHKESNDSCSG 1055

RESULT 2
ABU07847 standard; protein; 1055 AA.
ID ABU07847
XX AC ABU07847;
XX DT 10-MAY-2003 (first entry)
XX DE Human ephrin receptor ligand EphB2.
XX KW Cytostatic; vasodilator; antiinflammatory; cardiact; gene therapy;
KW ligand-receptor binding modulator; ephrin ligand; angiogenesis;
KW lymphangiogenesis; aberrant Ephrin-Tie biology; cell growth disorder;
KW cell migration disorder; cell proliferation disorder; neovascularisation;
KW ischaemia; infarction; tissue graft; transplant; human;
KW ephrin receptor ligand; tie receptor tyrosine kinase; EphB2.
XX OS Homo sapiens.
XX PN MO2003004523-AA2.
XX PD 16-JAN-2003.
XX PF 02-JUL-2002; 2002WO-IB002524.
XX PR 02-JUL-2001; 2001US-0302960P.
XX RA (LICN) LICENTIA LTD.
XX PI Aitalo K, Kubo H;

XX WP1, 2003-210341/20.
DR N-PSDB; ABX12548.
XX Identifying modulators of binding between a Tie receptor tyrosine kinase
PT and an Ephrin ligand, useful for promoting neovascularization, comprises
PT contacting a Tie receptor with an Ephrin in the presence of a putative
PT modulator.
XX Disclosure; Page 128-132; 199pp; English.
PS The invention describes a method of identifying a modulator of binding
XX between a Tie receptor tyrosine kinase and an Ephrin ligand. The method
CC comprises contacting a Tie receptor composition with an Ephrin
CC composition in the presence and in the absence of a putative modulator
CC compound, and detecting the binding between the receptor and the Ephrin
CC in the presence and in the absence of the putative modulator. The method
CC is useful for identifying a modulator of binding between a Tie receptor
CC tyrosine kinase and an Ephrin ligand. Modulators identified from the
CC method are useful in modulating angiogenic processes, including
CC lymphangiogenesis, for treating diseases associated with aberrant Ephrin-
CC Tie biology, aberrant growth, migration or proliferation of cells that
CC express a Tie receptor, or for promoting growth of vessel or
CC neovascularisation (e.g. ischaemic tissue, an infarction, a new or
CC chronic compound, or a tissue graft or transplant). This is the amino
CC acid sequence of human EphB2, a member of the Ephrin-B subfamily of
CC ligands that are bound to the membrane via a transmembrane domain and
CC short cytoplasmic tail and function as Ephrin receptor ligands
SQ Sequence 1055 AA.
Query Match 100.0%; Score 5571; DB 6; Length 1055;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1055; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALRRLGALLLPLAAVEETLMDSTTATAEIGMWHYPPSGWEVSGYDENNTIRTYQ 60
Db 1 MALRRLGALLLPLAAVEETLMDSTTATAEIGMWHYPPSGWEVSGYDENNTIRTYQ 60
QY 61 VCNVFESSQNNWLTKEIRRRGARHIVEMKFSYRDCSSIPSYGSCKETFNLYYEADF 120
Db 61 VCNVFESSQNNWLTKEIRRRGARHIVEMKFSYRDCSSIPSYGSCKETFNLYYEADF 120
QY 121 DSATKTFPNNMENWVYDITIADESFSQVDLGRVWKITETVRSFGVRSQGYLAPOD 180
Db 121 DSATKTFPNNMENWVYDITIADESFSQVDLGRVWKITETVRSFGVRSQGYLAPOD 180
QY 121 DSATKTFPNNMENWVYDITIADESFSQVDLGRVWKITETVRSFGVRSQGYLAPOD 180
Db 121 DSATKTFPNNMENWVYDITIADESFSQVDLGRVWKITETVRSFGVRSQGYLAPOD 180
QY 181 YGCGMSLIAVVFYRKCPRIIQNGAIFQETLSGAEESTLVAARGSCIANAEVDPILKY 240
Db 181 YGCGMSLIAVVFYRKCPRIIQNGAIFQETLSGAEESTLVAARGSCIANAEVDPILKY 240
QY 241 CNGDGEWLVPIGRMCGAGFEAVENGTVCGCGSGGTFRKANOGDPACTHCHINRTSEGA 300
Db 241 CNGDGEWLVPIGRMCGAGFEAVENGTVCGCGSGGTFRKANOGDPACTHCHINRTSEGA 300
QY 301 TNCVGRAGYRADLDDPDMCTTIPSAPOAVISVNETSLMLMTPRDSDGREDLVYNI 360
Db 301 TNCVGRAGYRADLDDPDMCTTIPSAPOAVISVNETSLMLMTPRDSDGREDLVYNI 360
QY 361 ICXSCSGGRGACTRFGDGNVOYAPRQLGTPEPRIYISDLAHTQYTFPIQAVNGVTDOSP 420
Db 361 ICXSCSGGRGACTRFGDGNVOYAPRQLGTPEPRIYISDLAHTQYTFPIQAVNGVTDOSP 420
QY 421 SPOFASVNTTNOAPAVSIMEQVSRITDSTLSNSQDPQNGVILIDYELQYKEKLE 480
Db 421 SPOFASVNTTNOAPAVSIMEQVSRITDSTLSNSQDPQNGVILIDYELQYKEKLE 480
QY 481 YNATAIKSPNTVTVOGLKAGAIYVFOVARATVAGYGRYSGKXYFQMTAEAYQTSIOEK 540
Db 481 YNATAIKSPNTVTVOGLKAGAIYVFOVARATVAGYGRYSGKXYFQMTAEAYQTSIOEK 540
QY 541 LPLIGSSAGVFLIAVNVVIAIVCNRRGFERADSETYDLCQYTSGHMTPGKXIYDPF 600
Db 541 LPLIGSSAGVFLIAVNVVIAIVCNRRGFERADSETYDLCQYTSGHMTPGKXIYDPF 600

Db		541	LPLTIGSSAAALVFLIAVVAIVAIICNRRGRFRADSEYDCKQHVTYSGHNTPGMKIYIDPF	600
QY		601	TYEDPNEVREFAEIADISCKIEQVIGAGFEFVCSGHTLPGRRLEFVAIKTLKAGYT	660
Db		601	TYEDPNEVREFAEIADISCKIEQVIGAGFEFVCSGHTLPGRRLEFVAIKTLKAGYT	660
QY		661	EKQRDFLSEASIMGQFDHPVIVHLEGVYTKSTPYMITTEFMENGSLDSFLRQNDGQFTV	720
Db		661	EKQRDFLSEASIMGQFDHPVIVHLEGVYTKSTPYMITTEFMENGSLDSFLRQNDGQFTV	720
QY		721	IQLVGMIRGIAAGKXYLADNMYVHRDLAARILVNSNVCVYSDPGLSRFIEDTSDPTY	780
Db		721	IQLVGMIRGIAAGKXYLADNMYVHRDLAARILVNSNVCVYSDPGLSRFIEDTSDPTY	780
QY		781	TSALVGKIPIRWTAPEALIQYRKFTSAPDWSYGIYMEVMSYGERPYMDTNODYNAIE	840
Db		781	TSALVGKIPIRWTAPEALIQYRKFTSAPDWSYGIYMEVMSYGERPYMDTNODYNAIE	840
QY		841	QDYELPEPPMDCPSALHQLMDQWQZDRNRHPRKFGQIVNTLDMKIRNPNSLKAAAPLSSGI	900
Db		841	QDYELPEPPMDCPSALHQLMDQWQZDRNRHPRKFGQIVNTLDMKIRNPNSLKAAAPLSSGI	900
QY		901	NLPLLDRTIPRYTSFNIVDEWLEALIKKQYKESFANAQFTSPDYVSSQMMEDILAVGYTL	960
Db		901	NLPLLDRTIPRYTSFNIVDEWLEALIKKQYKESFANAQFTSPDYVSSQMMEDILAVGYTL	960
QY		961	AGHOKKILINSIQVRAQMNQIQSYEGQPLARPRATGRTRKQCPRDVYKTKCNSNDGKKX	1020
Db		961	AGHOKKILINSIQVRAQMNQIQSYEGQPLARPRATGRTRKQCPRDVYKTKCNSNDGKKX	1020
QY		1021	GMGKKKTDPGRGREIQGIFFEEDSHKESNDSCCG	1055
Db		1021	GMGKKKTDPGRGREIQGIFFEEDSHKESNDSCCG	1055
RESULT 3				
AAB19590				
ID	AAB19590	standard; protein; 987 AA.		
XX	XX			
AC	AAB19590;			
XX	XX			
DT	22-JAN-2001	(first entry)		
XX	XX			
DE	Human CASB616.			
XX	XX			
KW	CASB616; EPHB2; ERK; EPH3; EPH73; DRT; HEK5; EPHB2v;			
KM	receptor protein tyrosine kinase; human; antigen; colon cancer;			
KX	ovary cancer; tumour; autoimmune disease; vaccine; therapy; diagnosis.			
OS	Homo sapiens.			
XX	XX			
FX	Key	Location/Qualifiers		
FT	Misc-difference	568..569		
FT	FT	/note= "an additional Arg residue decodes from the		
FT	FT	CAS616 nucleotide sequence given in the specification		
FT	FT	(see AAA88548), but is not given in the CAS616 amino		
FT	FT	acid sequence in the specification"		
FT	Misc-difference	956		
FT	FT	/note= "encoded by GTT"		
XX	XX			
PN	W0200053216-A2.			
XX	XX			
PD	14-SEP-2000.			
XX	XX			
FE	28-FEB-2000; 2000MO-EP001587.			
XX	XX			
PR	05-MAR-1999; 99GB-00005124.			
XX	XX			
PA	(SMIK) SMITHKLINE BEECHAM BIOLOGICALS.			
XX	XX			
PI	Vinals y De BassolsC;			
XX	XX			
DR	WPI; 2000-587384/55.			

Query	March	92.8%	Score 5170.5	DB 3	Length 987
Best Local Similarity	99.8%	Pred. No. 0			
Matches 984	Conservative	1	Mismatches	0	Indels 1, Gaps 1
1	MAIRRGALLLLPLLAVEETLMDSTATAELGMVHPESGEVSGYDENNTIRTYQ	60			
1	MAIRRGALLLLPLLAVEETLMDSTATAELGMVHPESGEVSGYDENNTIRTYQ	60			
61	VCNVESSQNMVLRKIFRIRRGANHIVEMFSVRDSSIPSVSGSKETFNLYYEADP	120			
61	VCNVESSQNMVLRKIFRIRRGANHIVEMFSVRDSSIPSVSGSKETFNLYYEADP	120			
61	VCNVESSQNMVLRKIFRIRRGANHIVEMFSVRDSSIPSVSGSKETFNLYYEADP	120			
121	DSATKTFPMNMENPMWKVDTIADDSFSQVLDGRWKMINTEVSPGVRSGFYLAFO	180			
121	DSATKTFPMNMENPMWKVDTIADDSFSQVLDGRWKMINTEVSPGVRSGFYLAFO	180			
181	YGGGMSLLIARVYFRKCPRIIONGAIPOETLSCAESTSLVAARSCITANAEVDVPIKLY	240			
181	YGGGMSLLIARVYFRKCPRIIONGAIPOETLSCAESTSLVAARSCITANAEVDVPIKLY	240			
241	CNDDGEMVLPIRCCKCKGFEAVENGATVCRCPGTFKANGDCACTHCINSRTTSEGA	300			
241	CNDDGEMVLPIRCCKCKGFEAVENGATVCRCPGTFKANGDCACTHCINSRTTSEGA	300			
301	TNCVCNNGYRRADLDPLDMPCCTTISAPQAVIASSVNETSLMLEWTPRDSGREDIIVYNI	360			
301	TNCVCNNGYRRADLDPLDMPCCTTISAPQAVIASSVNETSLMLEWTPRDSGREDIIVYNI	360			
361	ICSCSGSGGACCTRCGDNOVQAPROLGLTERIYISDLIAHTQVTFPIQAVNGVTQSPR	420			
361	ICSCSGSGGACCTRCGDNOVQAPROLGLTERIYISDLIAHTQVTFPIQAVNGVTQSPR	420			
421	SPPFASNTITNOAAPSAYSIMHQSRIVDSITLWSQPDQPNVILADYELQYEXELSE	480			
421	SPPFASNTITNOAAPSAYSIMHQSRIVDSITLWSQPDQPNVILADYELQYEXELSE	480			
481	YNATAIKSPNTITVOGLKAGAIYFQVAPARTVAGYGRSGKMFQMTAEIQTSLQEK	540			
481	YNATAIKSPNTITVOGLKAGAIYFQVAPARTVAGYGRSGKMFQMTAEIQTSLQEK	540			
541	LPILIISSAAGVFLIAVVVIAIVON-BRGEPRADSEYTDLQHTYSGHTPMGKIYIDP	599			
541	LPILIISSAAGVFLIAVVVIAIVON-BRGEPRADSEYTDLQHTYSGHTPMGKIYIDP	599			
601	FTYEDPNEAVRSPAKEIDISCVKIQDVIAGCFEVSCHLKLPGKEIFVALIKTKSGY	659			
601	FTYEDPNEAVRSPAKEIDISCVKIQDVIAGCFEVSCHLKLPGKEIFVALIKTKSGY	659			
660	TEQRDRFLSEASIMVGFPHVHILDEGVYKSTPMVITTEFMNGSLDFILNQNGQFT	719			

Db 661 TEKQRDPLSEBASIMGQFDHPNVIHLGCVTKSTPVMIIIEFMENGLSDSFLRQNDQCF 720
 QY 720 VIOVLGMLRGIAGMKYLAQNNVYVRDLAARNTLVNSNLVCYKSDPGLSFLEDDTSDPT 779
 Db 721 VIOVLGMLRGIAGMKYLAQNNVYVRDLAARNTLVNSNLVCYKSDPGLSFLEDDTSDPT 780
 QY 780 YTSALGKRIPIRMTAPPAIYRKFTSADSVSYGYIMMEVMSYGERPPYMDTNQDVINAI 839
 Db 781 YTSALGKRIPIRMTAPPAIYRKFTSADSVSYGYIMMEVMSYGERPPYMDTNQDVINAI 840
 QY 840 EODRLEPPMDCPSEALHQLMLDCQKDRNRHPKGOIVNTLDKIRNPNSLKAMAPLSSG 899
 Db 841 EODRLEPPMDCPSEALHQLMLDCQKDRNRHPKGOIVNTLDKIRNPNSLKAMAPLSSG 900
 QY 900 INPPLDRTIPDYTSFNTVDEMLBAIKMGQKESFANAGFTSPDVYSQMMEDILRVGT 959
 Db 901 INPPLDRTIPDYTSFNTVDEMLBAIKMGQKESFANAGFTSPDVYSQMMEDILRVGT 960
 QY 960 LAGHOKILNSIQVMPAKNNQIOSVE 985
 Db 961 LAGHOKILNSIQVMPAKNNQIOSVE 986

RESULT 4
 ID AAM26366
 AAM26366 standard; protein; 994 AA.
 AC AAM26366;
 DT 02-DEC-1997 (first entry)
 XX
 DE Mouse Nuk tyrosine kinase.
 KW Nuk tyrosine kinase; Eph receptor tyrosine kinase; signal transduction;
 KW acronogenesis; neurodegenerative disease; Alzheimer's disease;
 KW Parkinson's disease; Huntington's disease; multiple sclerosis;
 KW amyotrophic lateral sclerosis; Wernicke's disease; nerve damage; trauma;
 KW ischaemia; stroke.
 XX
 OS Mus musculus.
 XX
 Key Location/Qualifiers
 FT Peptide 1..26
 FT /label= Sig_peptide
 FT Protein 27..994
 FT /label= Mat_protein
 FT Domain 27..548
 FT /label= Extracellular_domain
 FT Region 330..420
 FT /label= FNIII
 FT Region /note= "Fibronectin type III repeat"
 FT 444..534
 FT /label= FNIII
 FT /note= "Fibronectin type III repeat"
 FT 548..574
 FT /label= Transmembrane_domain
 FT Domain 575..994
 FT /label= Cytoplasmic_domain
 FT Region 623..888
 FT /label= Tyrosine-kinase_region
 PN MO9714966-A1.
 PD 24-APR-1997.
 XX
 PF 10-OCT-1996; 96WO-CA000679.
 XX
 PR 13-OCT-1995; 95US-0005518P.
 PA (MOUN) MOUNT SINAI HOSPITAL CORP.
 PI Pawsen A, Henkemeyer M;
 XX

DR WPI, 1997-245245/22.
 DR N-PSDB; AAT84528.
 PT Activation of ligand regulatory pathways by Eph subfamily receptor
 PT tyrosine kinases - for stimulating or inhibiting axonogenesis, useful for
 PT treatment of e.g. neurodegenerative diseases such as Alzheimer's or
 PT Parkinson's diseases.
 PS Disclosure; Fig 3; 55pp; English.
 XX
 CC Murine Nuk tyrosine kinase is an Eph subfamily receptor tyrosine kinase
 CC that is essential for formation of the medial tract of the anterior
 CC commissure of the brain, and which appears to play a role in the
 CC formation of the habenular interpeduncle tract. Its amino acid sequence
 CC was deduced from cDNA clones (see AAT84528) isolated from an embryo cDNA
 CC library. The extracellular domain of Nuk was shown to be sufficient for
 CC formation of the medial tract. Eph subfamily receptor tyrosine kinases
 CC (e.g. the Nuk extracellular domain) can be used in claimed methods to:
 CC activate a ligand regulatory pathway in a cell; identify substances able
 CC to bind a ligand for an Eph subfamily receptor tyrosine kinase; and to
 CC affect neuronal development or regeneration, especially the stimulation
 CC or inhibition of axonogenesis, in a mammal. Activation of the stimulation
 CC regulatory pathway results in downstream activation of a series of
 CC cytoskeletal architecture, cell metabolism, cell migration and cell-cell
 CC interactions. Substances which activate the ligand regulatory pathway may
 CC be used for stimulating or inhibiting neuronal development regeneration
 CC and axonal migration associated with neurodegenerative disease e.g.
 CC Alzheimer's, Parkinson's or Huntington's diseases, multiple sclerosis,
 CC amyotrophic lateral sclerosis, deficiency diseases such as Wernicke's
 CC disease, peripheral nerve damage, trauma and ischaemia resulting from
 CC stroke
 CC
 SQ Sequence 994 AA;
 Query Match 92.1%; Score 5129; DB 2; Length 994;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 972; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 10 LLLPLLAAYEETIMDSITTAETLGGMVHPSPGMEVSYGDENNTIRTYQCVNPESSQ 69
 Db 18 LLLPLLAAYEETIMDSITTAETLGGMVHPSPGMEVSYGDENNTIRTYQCVNPESSQ 77
 QY 70 NNWLRTKFIIRRGARHRIHVEKESVVDSSIPSPGSKETPNLYYEADFDATKTFPN 129
 Db 78 NNWLRTKFIIRRGARHRIHVEKESVVDSSIPSPGSKETPNLYYEADFDATKTFPN 137
 QY 130 WMENPMVKVDTIADSEFSQVDJGGRYMKINTVRSRGPVRSRGPYAFADYGGCWSLIA 189
 Db 138 WMENPMVKVDTIADSEFSQVDJGGRYMKINTVRSRGPVRSRGPYAFADYGGCWSLIA 197
 QY 190 VRVFRKCPRIQNGAFQETLSGAEESTLVAARGSCINAAEEDVPIKLYCNGDGEMLV 249
 Db 198 VRVFRKCPRIQNGAFQETLSGAEESTLVAARGSCINAAEEDVPIKLYCNGDGEMLV 257
 QY 250 FIGRCYKAGFEAVENGTVRGCPSGTFKANKQGDDEACTHCPINSRITTSBATNVCVRNGY 309
 Db 258 FIGRCYKAGFEAVENGTVRGCPSGTFKANKQGDDEACTHCPINSRITTSBATNVCVRNGY 317
 QY 310 YRADLPDLPDMPCTTIPAPQAVTSVNETSLMTEMTPPRDSGREDLVNIIKSCGSGSR 369
 Db 318 YRADLPDLPDMPCTTIPAPQAVTSVNETSLMTEMTPPRDSGREDLVNIIKSCGSGSR 377
 QY 370 GACTRCGDNVQYAPRQGLTEPRYISDLIAHQYFEIQAQVGVTDQSPFSQFASVNI 429
 Db 378 GACTRCGDNVQYAPRQGLTEPRYISDLIAHQYFEIQAQVGVTDQSPFSQFASVNI 437
 QY 430 TTNGAASAVSIMHOVSRVTDSTLISGSDPDQNGVILDOYLYKEKEISEVNAATIKSP 489
 Db 438 TTNGAASAVSIMHOVSRVTDSTLISGSDPDQNGVILDOYLYKEKEISEVNAATIKSP 497
 QY 490 TTTVTVOGLKAGAIYVQVARTVAGYRGYSGMYFQMTAEAYQTSIOEKLPLIIGSSA 549

Db 498 TMTVTGGLKAGAIYFQVAPARTVAGYGRYSGKNYFQMTAEAYQTSIEKPLIVGSSA 557
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 Db 558 AGVFLIAVVVIAIVCNRRGFERADSEYTDKLOHTYSGHNTPMKRIYIDPFTYEDPNEAY 617
 QY 610 REPAKSIDISCVKIEQVIGAGFGEVCSGHLKPGREIFVAIKTLKSGYTEKORDEPLS 669
 Db 618 REPAKSIDISCVKIEQVIGAGFGEVCSGHLKPGREIFVAIKTLKSGYTEKORDEPLS 677
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 Db 678 EASIMQGFDPNVIHLEGVTKSTPWIITEPEMNSLDSFRRQNGQFTVILQVGMLEG 737
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 Db 738 IAAGMKYLDAMNYVHRDLAARNILVNSNLVCVSGFGLSRFLEDDTSDPTYSALGKIP 797
 QY 790 IRTTAPBAIORYKFTSADVWYSGIWMYMGYGERPYMDMTQDVINALI EODYRLPPM 849
 Db 798 IRTTAPBAIORYKFTSADVWYSGIWMYMGYGERPYMDMTQDVINALI EODYRLPPM 857
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 Db 858 DCPSSALHQLMLDCMQKDRNRPFGQIVNTLDMINPNLSLKMAAPLSSGINLPILDRIT 917
 QY 910 PDIYTSNTVDENIEMAIKMGQYKESFANAGFTSPDVVSQMMEDILKVGVTLAGHQKKILN 969
 Db 918 PDIYTSNTVDENIEMAIKMGQYKESFANAGFTSPDVVSQMMEDILKVGVTLAGHQKKILN 977
 QY 970 SIQVRAQNMQIOSVE 985
 Db 978 SIQVRAQNMQIOSVE 993
 RESULT 5
 AAU01907 ID AAU01907 standard; protein; 994 AA.
 AC AAU01907;
 XX
 DT 29-AUG-2001 (first entry)
 XX
 DE Murine neural kinase (Nuk) polypeptide.
 XX
 KM Neural kinase; Nuk; receptor tyrosine kinase; axonal migration; stroke;
 KM nerve fibre; cell-cell interaction; axonogenesis; neuronal development;
 KM regeneration; neurodegenerative disorder; Alzheimer's disease; ischemia;
 KM Parkinson's disease; Huntington's disease; demyelinating disease;
 KM multiple sclerosis; amyotrophic lateral sclerosis; deficiency disease;
 KM Wernicke's disease; nutritional polyneuropathy; multistem degeneration;
 KM progressive supranuclear palsy; Shy Drager's syndrome; mouse;
 KM olivoponto cerebellar atrophy; peripheral nerve damage.
 KM
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..26
 FT /note="Signal peptide"
 FT 26..548
 FT Domain
 FT /notes="Extracellular domain, preferably residues 26-548"
 FT 27..994
 FT Protein
 FT /note="Mature murine neural kinase"
 FT 52..119
 FT Domain
 FT /note="Ig-like domain"
 FT 239..268
 FT Region
 FT /note="Ig-like Nuk repeat"
 FT 330..420
 FT Region
 FT /note="Fibronectin type III repeat"
 FT 444..534
 FT Region
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 FT 549..574
 FT Domain
 FT /note="Hydrophobic transmembrane domain"

FT Binding-site 600..618
 FT /note="SH2 domain binding site"
 FT Region 601..994
 FT /note="Carboxy terminal"
 FT Modified-site 604..613
 FT /note="phosphorylation site"
 FT Domain 623..888
 FT /note="Catalytic tyrosine kinase domain"
 FT Binding-site 623..707
 FT /note="ATP binding site"
 PN US6218356-B1.
 PD 17-APR-2001.
 PF 13-OCT-1995; 95US-00542635.
 PR 29-APR-1994; 94US-00235407.
 PR 28-APR-1995; 95MO-CA000254.
 PA (MOUN) MOUNT SINAI HOSPITAL CORP.
 PI Pawson A, Henkemeyer M, Letwin K;
 XX WPI: 2001-289845/30.
 DR N-PSDB; AAS03812.
 PT New composition comprising neural receptor tyrosine kinase protein useful
 PT for inhibiting or stimulating axonogenesis, neuronal development, or
 XX regeneration and axonal migration.
 PS Claim 1; Fig 2; 86pp; English.
 CC The sequence represents a mouse neural kinase (Nuk) polypeptide. The
 CC murine Nuk locus has been mapped to the distal end of chromosome four.
 CC The polypeptide is a novel receptor tyrosine kinase protein, and is found
 CC to be expressed at high levels within migrating axons and is associated
 CC with nerve fibres. It functions to regulate specific cell-cell
 CC interactions during early development of the nervous system and in
 CC axonogenesis. Substances which bind to the Nuk protein, particularly
 CC ligands, may be used for stimulating or inhibiting neuronal development,
 CC regeneration and axonal migration associated with neurodegenerative
 CC disorders and conditions involving trauma and injury to the nervous
 CC system. These disorders include Alzheimer's disease, Parkinson's disease,
 CC Huntington's disease, demyelinating diseases such as multiple sclerosis,
 CC amyotrophic lateral sclerosis, deficiency diseases such as Wernicke's
 CC disease and nutritional polyneuropathy, progressive supranuclear palsy,
 CC Shy Drager's syndrome, multistem degeneration, olivoponto cerebellar
 CC atrophy, peripheral nerve damage, and ischemia resulting from stroke.
 CC The proteins may be used to prepare antibodies having specificity for Nuk
 CC proteins, which can be used to diagnose or treat disorders of the nervous
 CC system. These proteins are also used for screening agonists or
 CC antagonists of the interactions of the Nuk proteins with binding
 CC molecules
 CC
 SQ Sequence 994 AA;
 XX
 XX
 Query Match 92.1%; Score 5129; DB 4; Length 994;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 972; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 10 LILLPLLAVERETLMDSTTATAELGMYRPPSGMEVSGYENMTTITTYQVCVVFSSQ 69
 Db 18 LILLPLLAVERETLMDSTTATAELGMYRPPSGMEVSGYENMTTITTYQVCVVFSSQ 77
 QY 70 NNMLRTKXIRRRGARIRHVENKFSVRDCSSIPSPVSGSKETFNLYYYEADPSATKTPPN 129
 Db 78 NNMLRTKXIRRRGARIRHVENKFSVRDCSSIPSPVSGSKETFNLYYYEADPSATKTPPN 137
 QY 130 WMENPFWKYVDITIADESSQVDLGRVWKINTEVRSFSPVRSRGFYLAFOYGGMSILA 189
 Db 138 WMENPFWKYVDITIADESSQVDLGRVWKINTEVRSFSPVRSRGFYLAFOYGGMSILA 197

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Db 198 VRVFRKCPRIIONGALFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGMV 257
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Db 258 PIGCMCKAGFEAVENGTVCRGCGSGTFKXANOGDEACTHOPINSRTTSECATNCVCRNGY 317
QY 310 YRALDPLDMECTTIPAPQAVISSVNETSLMELWTPRPSGREDIVYNIICKSGSGR 369
Db 318 YRALDPLDMECTTIPAPQAVISSVNETSLMELWTPRPSGREDIVYNIICKSGSGR 377
QY 370 GACTRCGDNOYAPRQGLTEPRYISDLIAHQYFELIOAVNGVDQSPFSPQASVNI 429
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QY 430 TTNOAASAVSINHVSRTVDSITLSMSOPDONGVILDELQYEXEKLESEVATAIKSP 489
Db 438 TTNOAASAVSINHVSRTVDSITLSMSOPDONGVILDELQYEXEKLESEVATAIKSP 497
QY 490 TMTVTVOGLKAGALYFQVAPRTVAGYGRYSGMYFQMTAEAYQTSIOEKLPLITGSSA 549
Db 498 TMTVTVOGLKAGALYFQVAPRTVAGYGRYSGMYFQMTAEAYQTSIOEKLPLITGSSA 557
QY 550 AGVFLIAYVVIATVCCRGRBERADSEYTDKLOHYTSGHWTPOMKYIYDPFTYEDNEAV 609
Db 558 AGVFLIAYVVIATVCCRGRBERADSEYTDKLOHYTSGHWTPOMKYIYDPFTYEDNEAV 617
QY 610 REFAKEIDISCVKIEQYIGAGEFGEVCSGHLKPGKEIPLVAKITLKSQYTERORDFLS 669
Db 618 REFAKEIDISCVKIEQYIGAGEFGEVCSGHLKPGKEIPLVAKITLKSQYTERORDFLS 677
QY 670 EASIMGQFDHPNVIHLEGGVTKSPVMTITEFMENGLSDFLFQNGQFVIOLVGMIMG 729
Db 678 EASIMGQFDHPNVIHLEGGVTKSPVMTITEFMENGLSDFLFQNGQFVIOLVGMIMG 737
QY 730 IAAGMKTLADNMVYHRLAARNILVNSNLVCKVSDFLSFLDEDDPTYSALSGKIP 789
Db 738 IAAGMKTLADNMVYHRLAARNILVNSNLVCKVSDFLSFLDEDDPTYSALSGKIP 797
QY 790 IRMTAPAIQYRKFTASDVWSYGIYVMEVMSYGERPYDMNTQDVIYINAEODYRLPPM 849
Db 798 IRMTAPAIQYRKFTASDVWSYGIYVMEVMSYGERPYDMNTQDVIYINAEODYRLPPM 857
QY 850 DCSALHQLMDLDCQKORNRHPKFGQIVNTLDKINRPNLSKMAVPLSSGINLPLDRTI 909
Db 858 DCSALHQLMDLDCQKORNRHPKFGQIVNTLDKINRPNLSKMAVPLSSGINLPLDRTI 917
QY 910 PDYTSFNTVDEMLBAIKMGQYKESFANAGTSPDVVSQMMMEDILRVGYTLAGHQKILN 969
Db 918 PDYTSFNTVDEMLBAIKMGQYKESFANAGTSPDVVSQMMMEDILRVGYTLAGHQKILN 977
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Db 978 SIQVRAQNMQIOSVE 993

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FT Peptide
FT 1. .26
FT /label= Sig_peptide
FT 27. .548
FT Region
FT /label= Extracellular_region
FT /note= "the extracellular region (amino acids 27-548)
FT includes an N-terminal Ig-like domain and an Ig-like Nuk
FT repeat"
FT 330. .420
FT Region
FT /label= FNIII
FT /note= "fibronectin type III repeat"
FT 444. 534
FT Region
FT /label= FNIII
FT /note= "fibronectin type III repeat"
FT 549. .574
FT Region
FT /label= Transmembrane_region
FT 575. .594
FT Region
FT /label= Cytoplasmic_region
FT 623. 707
FT Domain
FT /label= Tyrosine-kinase_catalytic_domain
FT
FT W09530326-A1.
FT
FT 09-NOV-1995.
FT
FT 28-APR-1995; 95WO-C0000254.
FT
FT 29-APR-1994; 94US-00235407.
FT
FT (MOUN ) MOUNT SINAI HOSPITAL CORP.
FT
FT Pawson A, Henkemeyer M, Letwin K;
FT WPI. 1995-393299/50.
FT N-PSDB; AAT07308.
FT
FT DNA encoding neural receptor tyrosine kinase - useful in gene therapy of
FT nerve disorders, and for diagnosis and identification of therapeutic
FT agents.
FT
FT Claim 1: Page 70-74; 103pp; English.
FT
FT A novel receptor tyrosine kinase (AAR87018), designated neural kinase
FT (Nuk) (AAR87018), is encoded by cDNA (AAT07308) obtd. from a mouse embryo
FT library. Nuk is expressed in migrating axons and is involved in cell-cell
FT interactions and axogenesis in development of the nervous system. Nuk
FT or its fragments (pref. amino acids 26-548 or 601-994) are used to
FT identify (ant)agonists of the (activated) receptor tyrosine kinase as a
FT means of treating nerve disorders and damage, or to raise antibodies used
FT to monitor axon migration and nerve cell interactions
FT
FT Sequence 994 AA:
FT
FT Query Match 92.0%; Score 5125; DB 2; Length 994;
FT Best Local Similarity 99.5%; Pred. No. 0;
FT Matches 971; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 10 LLLPLLAAYEETLMDSTTATLGMVHPSPGNEEVSQYDENNTIRTYQCVNPFSSQ 69
Db 18 LLLPLLAAYEETLMDSTTATLGMVHPSPGNEEVSQYDENNTIRTYQCVNPFSSQ 77
QY 70 NNMILRTKFIIRRGARHIVHEKVFSDCCSIPSPGCKETFNLYYYEAFDQATKTFPN 129
Db 78 NNMILRTKFIIRRGARHIVHEKVFSDCCSIPSPGCKETFNLYYYEAFDQATKTFPN 137
QY 130 WMENPWYKVDITIADESFQVDLGRVMKINTEVRSGFPVSRSGFYLAPODYGGCMSLIA 189
Db 138 WMENPWYKVDITIADESFQVDLGRVMKINTEVRSGFPVSRSGFYLAPODYGGCMSLIA 197
QY 190 VRVFRKCPRIIONGALFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGMV 249
Db 198 VRVFRKCPRIIONGALFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGMV 257
QY 250 PIGCMCKAGFEAVENGTVCRGCGSGTFKXANOGDEACTHOPINSRTTSECATNCVCRNGY 309

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Db 258 PIGCMCKAGFAEAVNGTVCRGCPGTFKANOQDEACTHCPINSTRTSECATNCVRNRY 317
QY 310 YRADLDLDMPCTTISAPQAVISVNETSLMLEMTPPRDSDGEREDLVYNIICKSGSGR 369
Db 318 YRADLDLDMPCTTISAPQAVISVNETSLMLEMTPPRDSDGEREDLVYNIICKSGSGR 377
QY 370 GACTRCGDNVQYAPROLGLTEPRITISDLLAHTQYTFEIOAVNGVTDQSPFQFASVNI 429
Db 378 GACTRCGDNVQYAPROLGLTEPRITISDLLAHTQYTFEIOAVNGVTDQSPFQFASVNI 437
QY 430 TTMQAPSAVSIMQVSRITVDSITLMSQPDQPNQVILDELYQYKEKSEYNATIKSP 489
Db 438 TTMQAPSAVSIMQVSRITVDSITLMSQPDQPNQVILDELYQYKEKSEYNATIKSP 497
QY 490 TMTVTQGLKAGAIYFQVARTVAGYGRYSGMVFQMTAEAYQTSIOEKLPLIIGSSA 549
Db 498 TMTVTQGLKAGAIYFQVARTVAGYGRYSGMVFQMTAEAYQTSIOEKLPLIIGSSA 557
QY 550 AGVFLIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPFYEDNEAV 609
Db 558 AGVFLIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPFYEDNEAV 617
QY 610 REPAKEIDISCVIEQYIGAGEFGEVCSGHLKPGKREIFVAIKTKSGYTEKQRDPIS 669
Db 618 REPAKEIDISCVIEQYIGAGEFGEVCSGHLKPGKREIFVAIKTKSGYTEKQRDPIS 677
QY 670 EASIMGQFDHPNVIHLEGVTKSTPVMITTEPMENGLDSFLRQNDQCFITQIVGMIRG 729
Db 678 EASIMGQFDHPNVIHLEGVTKSTPVMITTEPMENGLDSFLRQNDQCFITQIVGMIRG 737
QY 730 IAAQMKYLAQMYVHRDLAARNILVNSNLYCKVSDGLASPLEDDTSDPYTSALGCKLP 789
Db 738 IAAQMKYLAQMYVHRDLAARNILVNSNLYCKVSDGLASPLEDDTSDPYTSALGCKLP 797
QY 790 IRTWAPBAIQRKFTSASDVMSYGIWMEVMSYGERPMDTINQDIINAIEDYRLPPPM 849
Db 798 IRTWAPBAIQRKFTSASDVMSYGIWMEVMSYGERPMDTINQDIINAIEDYRLPPPM 857
QY 850 DCSALHQLMLDCMQCDNRHRPKFGQIVNLDKXINRPNLSLKAMAPLSSGINPLIDRTI 909
Db 858 DCSALHQLMLDCMQCDNRHRPKFGQIVNLDKXINRPNLSLKAMAPLSSGINPLIDRTI 917
QY 910 PDTSFTVDEMLEAIKMGQYKESFANAGFTSPDVSSQMMEDILRVGVTLAGHCKKILN 969
Db 918 PDTSFTVDEMLEAIKMGQYKESFANAGFTSPDVSSQMMEDILRVGVTLAGHCKKILN 977
QY 970 SIQVMAQMNQIOSVE 985
Db 978 SIQVMAQMNQIOSVE 993

RESULT 7
AAR85089
ID AAR85089 standard; protein; 970 AA.
XX AAR85089;
AC AAR85089;
XX
DT 16-APR-1996 (first entry)
XX
DE EPH-like receptor protein tyrosine kinase HEK5.
XX
XX EPH-like receptor protein tyrosine kinase; PK; HEK5;
KM human eph-like kinase; therapy; diagnosis; vector; antibody.
XX
XX Homo sapiens.
XX
XX W09528484-A1.
XX
XX 26-OCT-1995.
XX
XX 14-APR-1995; 95MO-US004681.
XX

PR 15-APR-1994; 94US-00229509.
XX
XX (AMGE-) AMGEN INC.
XX
XX Fox GM, Welcher AA, Jing S;
PI
XX WPI: 1995-373799/48.
DR
XX N-PSDB; AA02946.
DR
XX
XX New nucleic acid encoding EPH-like receptor tyrosine kinase(s) - and
PT related vectors, host cells, proteins, antibodies etc., used
PT diagnostically and therapeutically to modulate receptor activation or
PT prodn.
XX
XX Claim 18; Page 46-49; 133pp; English.
XX
XX 4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7,
CC HEK8 and HEK11 (AAR85089-92), respectively, were identified following
CC isolation of their encoding cDNAs (AA02946-49) from a human foetal brain
CC cDNA library. HEK5, HEK7 and HEK8 show extensive homology to the
CC catalytic domain of chicken EPH-like receptors Cek5, Cek7 and Cek8. HEK11
CC shows no homology to any known EPH-like receptor. Recombinant HEK
CC receptors (or their soluble extracellular domains) are produced by
CC expression of encoding sequences in prokaryotic or eucaryotic host cells,
CC and are used to produce antibodies (utilised in diagnostic assays) or to
CC identify and purify ligands for HEK receptors, or therapeutically to
CC modulate the activation of cell-associated receptors. Soluble HEK5
CC receptor may affect primarily brain and pancreatic cells
XX
SQ Sequence 970 AA;
Query Match 91.4%; Score 5092; DB 2; Length 970;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 967; Conservative 1; Mismatches 1; Indels 2; Gaps 1;
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Db 1 LIAAVEETLMDSTTATAEIAGMNVHBPSSGMEVSGYDENMNTIRTYQVNVFESSQNNMLR 60
QY 75 TKFIRRRGAHRIHVMKRSVYRDCSSIPSPVPSCKETFNLYYYEADPDSATYTFPMWMPNP 134
Db 61 TKFIRRRGAHRIHVMKRSVYRDCSSIPSPVPSCKETFNLYYYEADPDSATYTFPMWMPNP 120
QY 135 WKVVDITIADESFSQVDIGGRVWKINTEVRSFGFVRSRGFLAODYGGCSLAIARVYF 194
Db 121 WKVVDITIADESFSQVDIGGRVWKINTEVRSFGFVRSRGFLAODYGGCSLAIARVYF 180
QY 195 RKCPRIIONGAIFOETLSGAESTLSVAARSGCINAAEEVDVPIKLYCNGDEMLVPIRC 254
Db 181 RKCPRIIONGAIFOETLSGAESTLSVAARSGCINAAEEVDVPIKLYCNGDEMLVPIRC 240
QY 255 MCKAGFEAVNGTVCRGCPGTFKANOQDEACTHCPINSTRTSECATNCVRNRYRADL 314
Db 241 MCKAGFEAVNGTVCRGCPGTFKANOQDEACTHCPINSTRTSECATNCVRNRYRADL 300
QY 301 DELDMPCTTISAPQAVISVNETSLMLEMTPPRDSDGEREDLVYNIICKSGSGGACTR 360
Db 315 DELDMPCTTISAPQAVISVNETSLMLEMTPPRDSDGEREDLVYNIICKSGSGGACTR 374
QY 375 CGDNVQYAPROLGLTEPRITISDLLAHTQYTFEIOAVNGVTDQSPFQFASVNIITNQQA 434
Db 361 CGDNVQYAPROLGLTEPRITISDLLAHTQYTFEIOAVNGVTDQSPFQFASVNIITNQQA 420
QY 435 AFSASIMQVSRITVDSITLMSQPDQPNQVILDELYQYKEKSEYNATIKSPNTVT 494
Db 421 AFSASIMQVSRITVDSITLMSQPDQPNQVILDELYQYKEKSEYNATIKSPNTVT 480
QY 495 VQGLKAGAIYFQVARTVAGYGRYSGMVFQMTAEAYQTSIOEKLPLIIGSSAAGLVF 554
Db 481 --GLKAGAIYFQVARTVAGYGRYSGMVFQMTAEAYQTSIOEKLPLIIGSSAAGLVF 538
QY 555 LIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPFYEDNEAVREFAK 614

Db 539 LIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHITPGMKIYIDPFTYEDPNEAVREFAK 598
QY 615 EIDISCVKIQVIGAGFFGVCSGHLKLGKREIFVAIKTLKSGYTEKORDFLEASIM 674
Db 599 EIDISCVKIQVIGAGFFGVCSGHLKLGKREIFVAIKTLKSGYTEKORDFLEASIM 658
QY 675 GQFDHPVVIHLEGVVTKSTPVMITTEFMENGSLDSFLRQNDGQFTVQLVGMRLGIAAGM 734
Db 659 GQFDHPVVIHLEGVVTKSTPVMITTEFMENGSLDSFLRQNDGQFTVQLVGMRLGIAAGM 718
QY 735 KYLDADNMYVHRDLAARNILVNSNLVCKVSPFGLSRFLEDDTSPTYSALGKIPIRMTA 794
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QY 795 PEAIQYRKFTSASDVMSYGIWMMEVMSYGERPYWDMTNQDVINAIEQDYRLPPMDCPSA 854
Db 779 PEAIQYRKFTSASDVMSYGIWMMEVMSYGERPYWDMTNQDVINAIEQDYRLPPMDCPSA 838
QY 855 LHQIMLDCWQXDRNHRKFGQIVNTLDKXIRNPNSLKAMAPLSSGINLPILDRITPDYTS 914
Db 839 LHQIMLDCWQXDRNHRKFGQIVNTLDKXIRNPNSLKAMAPLSSGINLPILDRITPDYTS 898
QY 915 FNTVDWLEAIKMGQYKESFANAGFTSFVVSQMMEDILRVGVTLAGHOKKILNSIQVM 974
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QY 975 RAQNMNOIQSYE 985
Db 959 RAQNMNOIQSYE 969

Search completed: August 28, 2004, 04:08:46
Job time : 106.415 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2004, 04:05:25 ; Search time 24.814 Seconds
(without alignments)
2195.179 Million cell updates/sec

Title: US-09-914-883-4

Perfect score: 5571

Sequence: 1 MARRRGAALLLLPLLAAYE.....QGIFKEDSHKESNDSCSG 1055

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 90%
Maximum Match 100%
Listing first 45 summaries

Database:

Issued Patents_AA:*
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
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6: /cgn2_6/prodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5129	92.1	994	3	US-08-542-635-2
2	5092	91.4	970	2	US-08-449-645A-11
3	5092	91.4	970	2	US-08-702-367A-11
4	5092	91.4	970	5	PCT-US95-04681-11

ALIGNMENTS

RESULT 1
US-08-542-635-2
Sequence 2, Application US/08542635
Patent No. 6218356
GENERAL INFORMATION:
APPLICANT: Pawson, Anthony
APPLICANT: Henkemeyer, Mark
APPLICANT: Lecwin, Kenneth
TITLE OF INVENTION: NOVEL NEURAL RECEPTOR
TITLE OF INVENTION: TYROSINE KINASE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Bereskin & Parr
STREET: 40 King Street West, Box 401
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/542,635
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mediamid, Shona S.
REGISTRATION NUMBER: 38,798
REFERENCE/DOCKET NUMBER: 3153-162
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
TELEX: 06-23115
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 994 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Mus musculus
DEVELOPMENTAL STAGE: Embryo
IMMEDIATE SOURCE:
LIBRARY: lambda gtl0 cDNA library
CLONE: Combined pNKRACE A2 and K2 and cDNA clones
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Distal end of chromosome 4
MAP POSITION: near the and-1 mutation
US-08-542-635-2

Query Match          92.1%; Score 5129; DB 3; Length 994;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 972; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

10 LLLPLLAABETLMDSTATATAGLGMVHPSPGMEVSGYDENNTRTTYOVAVFEBSQ 69
18 LLLPLLAABETLMDSTATATAGLGMVHPSPGMEVSGYDENNTRTTYOVAVFEBSQ 77
70 NNMWRTKPIRRRGARHIVENKFSVRDSSIPSVGSKETFNLYYYHADPDAITKTFPN 129
78 NNMWRTKPIRRRGARHIVENKFSVRDSSIPSVGSKETFNLYYYHADPDAITKTFPN 137
130 WMENWVAVVDITLADDESFOVDLGRVWKINTVEVRSFGFVRSRGFYLAFOYGGMSLIA 189
138 WMENWVAVVDITLADDESFOVDLGRVWKINTVEVRSFGFVRSRGFYLAFOYGGMSLIA 197
190 VVVFYRKCPRIIONGALFOETLSGAEISTLVAAAGSCIANAEVDPKILYCNBGEWLV 249
198 VVVFYRKCPRIIONGALFOETLSGAEISTLVAAAGSCIANAEVDPKILYCNBGEWLV 257
250 PIGRCMCTAGFEAVENGVCGCGSRTFKANOGDEACTHCINRTTSEGTNCVCRNGY 309
258 PIGRCMCTAGFEAVENGVCGCGSRTFKANOGDEACTHCINRTTSEGTNCVCRNGY 317
310 YRADLDPDMCTTTPSAPOAVISSVNETSLMLBMTPPRDSGREDLVYNIICKSCGSGR 369
318 YRADLDPDMCTTTPSAPOAVISSVNETSLMLBMTPPRDSGREDLVYNIICKSCGSGR 377
370 GACTRCGNVOYAPBQCLTEPRITYISDLAHTQYTFEIOAVNGVTDOSPSPPOFASVNI 429
378 GACTRCGNVOYAPBQCLTEPRITYISDLAHTQYTFEIOAVNGVTDOSPSPPOFASVNI 437
430 TTNOAPSAVSIIMOVSRVDSITLSWQPDQPGVILIDYLOYYEKLSSEYNATKISP 489
438 TTNOAPSAVSIIMOVSRVDSITLSWQPDQPGVILIDYLOYYEKLSSEYNATKISP 497
490 TMTVTVGILKAGAIYVFOVRAATVAGVYSGKMYFQMTAEVQTSIQEKLPLIIGSSA 549
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Db 498 TNYTVVGLAGALIVFQVAVARTVAGYGRYSCKYFQYMTAEAYOTSIXEKLPLIYGSSA 557
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Db 558 AGVFLIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPFYEDPNEAV 617
QY 610 REPAKEIDISGVKEGVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORDPFS 669
Db 618 REPAKEIDISGVKEGVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORDPFS 677
QY 670 EASIMGQFDPHNVILHEGVVTKSTPVMIIIEFMENGLSDSFLRQNDGQFTVIQVLMRG 729
Db 678 EASIMGQFDPHNVILHEGVVTKSTPVMIIIEFMENGLSDSFLRQNDGQFTVIQVLMRG 737
QY 730 IAGMKYLAAMNYHRLAARNILVNSNLVCXSDGLSFLEDDTSDPTYSALGKLP 789
Db 738 IAGMKYLAAMNYHRLAARNILVNSNLVCXSDGLSFLEDDTSDPTYSALGKLP 797
QY 790 IRMTAPAIQYRKFTSASDVMSYGIWMEVMSYGERPYDMTNQDVINAIEDYRLPPPM 849
Db 798 IRMTAPAIQYRKFTSASDVMSYGIWMEVMSYGERPYDMTNQDVINAIEDYRLPPPM 857
QY 850 DCSBALHQLMDCWQDRNRHPRKFGQIVNTLDKMRNPNSLKMAFLSSGINLPLDRTI 909
Db 858 DCSBALHQLMDCWQDRNRHPRKFGQIVNTLDKMRNPNSLKMAFLSSGINLPLDRTI 917
QY 910 PDYTSFNTVDEWLEAIKMGQYKESFANAGFTSPDVVSQMMMEDILRVGVTLAGHQKILN 969
Db 918 PDYTSFNTVDEWLEAIKMGQYKESFANAGFTSPDVVSQMMMEDILRVGVTLAGHQKILN 977
QY 970 SIQVRAQNNQIOSVE 985
Db 978 SIQVRAQNNQIOSVE 993

RESULT 2

US-08-449-645A-11
Sequence 11, Application US/08449645A
Patent No. 5981245
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1840 Dehavenland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,645A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-449-645A-11

Query March 91.4%; Score 5093; DB 2; Length 970;
Best Local Similarity 99.6%; Pred. No. 0;

Matches 967; Conservative 1; Mismatches 1; Indels 2; Gaps 1;
QY 15 LIAAEEETLMDSTTAIAELGMVHPPSGMEVSGYDENMTIRIYQVCNPFESSQNNWLR 74
Db 1 LIAAEEETLMDSTTAIAELGMVHPPSGMEVSGYDENMTIRIYQVCNPFESSQNNWLR 60
QY 75 TKFIRRGCAHIHEMFMFSVDCSSIPSPVSCKETENLYYEAADPDSAKTFPFNMENP 134
Db 61 TKFIRRGCAHIHEMFMFSVDCSSIPSPVSCKETENLYYEAADPDSAKTFPFNMENP 120
QY 135 WKVYDTIADESFQVLDIGRWKINTEVRSFGFVSRSSGFYLAFODYGCMSLIAVEFY 194
Db 121 WKVYDTIADESFQVLDIGRWKINTEVRSFGFVSRSSGFYLAFODYGCMSLIAVEFY 180
QY 195 RKCPRIIONGAIPEETLSGAESTSLVAARSGCINNAEVEVPKILYCNBGEMLVPGRG 254
Db 181 RKCPRIIONGAIPEETLSGAESTSLVAARSGCINNAEVEVPKILYCNBGEMLVPGRG 240
QY 255 MCKAGFEAVENGIVCRGPGSGTFKRNQDEACTHCPINSRTTSGATNCVCRNGYRADL 314
Db 241 MCKAGFEAVENGIVCRGPGSGTFKRNQDEACTHCPINSRTTSGATNCVCRNGYRADL 300
QY 315 DPLMPCTTISAPQAVIISVNETSLMLEWTPPRDSGREDLVYNIICXSGSGRGACTR 374
Db 301 DPLMPCTTISAPQAVIISVNETSLMLEWTPPRDSGREDLVYNIICXSGSGRGACTR 360
QY 375 CGDNVQAPRQLGLTEPRIVISDLAHTOYTFEIOAVNGVTDOSPFSPQASVNIITNQA 434
Db 361 CGDNVQAPRQLGLTEPRIVISDLAHTOYTFEIOAVNGVTDOSPFSPQASVNIITNQA 420
QY 435 APSASVIMHQVSRVDSITLSKSPDPNGVILDYELQYKEKEISENATAIKSPMTYV 494
Db 421 APSASVIMHQVSRVDSITLSKSPDPNGVILDYELQYKEKEISENATAIKSPMTYV 480
QY 495 VQGLKAGIYVFOYRARTVAGYGRYSCKMYFQMTTEAYOTSIOEKLPLIIGSSAGLVF 554
Db 481 --GLKAGIYVFOYRARTVAGYGRYSCKMYFQMTTEAYOTSIOEKLPLIIGSSAGLVF 538
QY 555 LIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPFYEDPNEAVREFAK 614
Db 539 LIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPFYEDPNEAVREFAK 598
QY 615 EIDISCVKIEGVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORDFLSEASIM 674
Db 599 EIDISCVKIEGVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORDFLSEASIM 658
QY 675 GQFHPNVILHEGVVTKSTPVMIIIEFMENGLSDSFLRQNDGQFTVIQVLMRGIAAGM 734
Db 659 GQFHPNVILHEGVVTKSTPVMIIIEFMENGLSDSFLRQNDGQFTVIQVLMRGIAAGM 718
QY 735 KYLADNMVYHRLAARNILVNSNLVCXSDGLSFLEDDTSDPTYSALGKLPIMRTA 794
Db 719 KYLADNMVYHRLAARNILVNSNLVCXSDGLSFLEDDTSDPTYSALGKLPIMRTA 778
QY 795 PEAIQYRKFTSASDVMSYGIWMEVMSYGERPYDMTNQDVINAIEDYRLPPMDCPSA 854
Db 779 PEAIQYRKFTSASDVMSYGIWMEVMSYGERPYDMTNQDVINAIEDYRLPPMDCPSA 838
QY 855 LHQIMLDCWQDRNRHPRKFGQIVNTLDKMRNPNSLKMAFLSSGINLPLDRTIPYTS 914
Db 839 LHQIMLDCWQDRNRHPRKFGQIVNTLDKMRNPNSLKMAFLSSGINLPLDRTIPYTS 898
QY 915 FNTVDEWLEAIKMGQYKESFANAGFTSPDVVSQMMMEDILRVGVTLAGHQKILNIOVM 974
Db 899 FNTVDEWLEAIKMGQYKESFANAGFTSPDVVSQMMMEDILRVGVTLAGHQKILNIOVM 956
QY 975 RAQNNQIOSVE 985
Db 959 RAQNNQIOSVE 969

RESULT 3
US-08-702-367A-11

Sequence 11, Application US/08702367A
Patent No. 5991246
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1640 Dehaven Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,367A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-702-367A-11

Query Match 91.4%; Score 5092; DB 2; Length 970;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 967; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 15 LLAVEETLMDSTTAATAEIGMWHPPSGMEVSGYDENMATTRTTYVCNVPFSSQNNMLR 74
DB 1 LLAVEETLMDSTTAATAEIGMWHPPSGMEVSGYDENMATTRTTYVCNVPFSSQNNMLR 60
QY 75 TKFIRRGARHIVENKESFVDCSSIPSVGSGKETFNLYYEADDSATKTFPMNMEHP 134
DB 61 TKFIRRGARHIVENKESFVDCSSIPSVGSGKETFNLYYEADDSATKTFPMNMEHP 120
QY 135 WVKVDITIADESHSOVDLGRVWKNITEVRSFGVRSRSGFYLAFOYGGCMSLIAVRFY 194
DB 121 WVKVDITIADESHSOVDLGRVWKNITEVRSFGVRSRSGFYLAFOYGGCMSLIAVRFY 180
QY 195 RKPRRIIONGAIQOETLSGABESTLVAARSGCTANAEVDVPIKXYCNGDGEVLVPIGSC 254
DB 181 RKPRRIIONGAIQOETLSGABESTLVAARSGCTANAEVDVPIKXYCNGDGEVLVPIGSC 240
QY 255 MCRAGEAENVGTVCGCPGSGTFKANOGDEACTHCPIINSTRTSEGATNCVRNGYRADL 314
DB 241 MCRAGEAENVGTVCGCPGSGTFKANOGDEACTHCPIINSTRTSEGATNCVRNGYRADL 300
QY 315 DPLDMPCTTTPSAPOAVISVNETSLMLENTPPRDSGGRDLVYNTICSCSGGRACR 374
DB 301 DPLDMPCTTTPSAPOAVISVNETSLMLENTPPRDSGGRDLVYNTICSCSGGRACR 360
QY 375 CGDNVOYAPQOLGTERIYISDLAHTQYTFEIOANGVTPDOSPPSPQASVNTITNOA 434
DB 361 CGDNVOYAPQOLGTERIYISDLAHTQYTFEIOANGVTPDOSPPSPQASVNTITNOA 420
QY 435 APSAASIMHGVSRVDSITLSWQPDQPNGVIIIDYELQYVEKLSSEYNATAIKSPNTVT 494
DB 421 APSAASIMHGVSRVDSITLSWQPDQPNGVIIIDYELQYVEKLSSEYNATAIKSPNTVT 480
QY 495 VOGKKAIVFOYRAATVAGYRGSGMYFQMTAEVQTSIOEKLPLITGSAAGLV 554
DB 481 VOGKKAIVFOYRAATVAGYRGSGMYFQMTAEVQTSIOEKLPLITGSAAGLV 538

QY 555 LIAVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPEMKIYIDPFTYEDPNEAVREFAK 614
DB 539 LIAVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPEMKIYIDPFTYEDPNEAVREFAK 598
QY 615 EIDISCVKIEQVITAGFGEVCSGHLKLPGRREIFVAIKLKSGYTKORRDFLSEASIM 674
DB 599 EIDISCVKIEQVITAGFGEVCSGHLKLPGRREIFVAIKLKSGYTKORRDFLSEASIM 658
QY 675 GQFHPNVVHLEGVVTSTPMITTEPMENGSLDSFLRNDGQFTVQLVGMRLGIAAG 734
DB 659 GQFHPNVVHLEGVVTSTPMITTEPMENGSLDSFLRNDGQFTVQLVGMRLGIAAG 718
QY 735 KYLADNVYHEDLAARNILVNSNLCKVSPGLSRFLEDTSPTYSALGKPIRWTA 794
DB 719 KYLADNVYHEDLAARNILVNSNLCKVSPGLSRFLEDTSPTYSALGKPIRWTA 778
QY 795 PEAIQYRKFTSASVWSYGIWMEVMSYGRPYMDTNODVINAIEDGYRLPPMDCPSA 854
DB 779 PEAIQYRKFTSASVWSYGIWMEVMSYGRPYMDTNODVINAIEDGYRLPPMDCPSA 838
QY 855 LHQMLDCWQKDRNHRPFQIVNTLDKXIRNPNSLKAMAPLSSGINLPLDRTIPTYTS 914
DB 839 LHQMLDCWQKDRNHRPFQIVNTLDKXIRNPNSLKAMAPLSSGINLPLDRTIPTYTS 898
QY 915 FNTYDEMLBAIKGQYKESFANAGFTSFQDVYSQMMEDILRVGYTLAHHQKILINSIQM 974
DB 899 FNTYDEMLBAIKGQYKESFANAGFTSFQDVYSQMMEDILRVGYTLAHHQKILINSIQM 958
QY 975 RAQNNQIOSVE 985
DB 959 RAQNNQIOSVE 969

RESULT 4
PCT-US95-04681-11
Sequence 11, Application PC/TUS9504681
GENERAL INFORMATION:

APPLICANT: Fox, Gary M.
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1640 Dehaven Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04681
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04681-11

Query Match 91.4%; Score 5092; DB 5; Length 970;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 967; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 15 LLAABEETLMDSTTATAEALGMVHPSPGMEVSGYDENMNTIRTYOVCVNFESSQNNMLR 74
Db 1 LLAABEETLMDSTTATAEALGMVHPSPGMEVSGYDENMNTIRTYOVCVNFESSQNNMLR 60
QY 75 TKFIRRGARIRIHVEMKFSVRDCSITPSVPSCKEFTNLYYEADFDSATKTPNMENP 134
Db 61 TKFIRRGARIRIHVEMKFSVRDCSITPSVPSCKEFTNLYYEADFDSATKTPNMENP 120
QY 135 WVKVDTIADESFQVDLGRVWKINTEVASFGVSRSGFYLAFODYGGMSLIAVRFY 194
Db 121 WVKVDTIADESFQVDLGRVWKINTEVASFGVSRSGFYLAFODYGGMSLIAVRFY 180
QY 195 RKCRRITQNGAIFQETISGABSTSLVAARSGCIANAEVDVPIKLYCNGDEWLPVIGRC 254
Db 181 RKCRRITQNGAIFQETISGABSTSLVAARSGCIANAEVDVPIKLYCNGDEWLPVIGRC 240
QY 255 MCKAGFEAVENGTVCRGCPSGTFRKANGDEACTHCPINSRTSEGATNCVCRRNGYRADL 314
Db 241 MCKAGFEAVENGTVCRGCPSGTFRKANGDEACTHCPINSRTSEGATNCVCRRNGYRADL 300
QY 315 DPLDMPCTTIPSAPOAVISSVNETSLMLEWTPRDSGGREDLVYNIICKSCSGRGACTR 374
Db 301 DPLDMPCTTIPSAPOAVISSVNETSLMLEWTPRDSGGREDLVYNIICKSCSGRGACTR 360
QY 375 CGDNVOYAPROGLTEPRYISDLIAHTQYTFEIOANGVTQSPSPQFASVNIITNOA 434
Db 361 CGDNVOYAPROGLTEPRYISDLIAHTQYTFEIOANGVTQSPSPQFASVNIITNOA 420
QY 435 APSAVSIMHOVSRTVDSITLSMSQDPQPNVILDYELQYKEKELSEYNATAIKSPNTVT 494
Db 421 APSAVSIMHOVSRTVDSITLSMSQDPQPNVILDYELQYKEKELSEYNATAIKSPNTVT 480
QY 495 VOGIKGAIYVPOVARTVAGYRGYSKXYFOJTEAEVOTSIQEKPLIIGSSAGIYF 554
Db 481 - -GLKAGAIYVPOVARTVAGYRGYSKXYFOJTEAEVOTSIQEKPLIIGSSAGIYF 538
QY 555 LIAVVYIAIVCNRRGERADSEYTDKLOHYTSGMTPGMKIYIDPTYEDPNEAVNEPAK 614
Db 539 LIAVVYIAIVCNRRGERADSEYTDKLOHYTSGMTPGMKIYIDPTYEDPNEAVNEPAK 598
QY 615 EIDISCVKIEQVIGAGEFVCGSHLKLPGKREIFVAIKTLKSGYTEKORPFLSEASIM 674
Db 599 EIDISCVKIEQVIGAGEFVCGSHLKLPGKREIFVAIKTLKSGYTEKORPFLSEASIM 658
QY 675 GQPDHPVILHEGVVKTSPVMIITEFMENGSLDSFLRQNDQGFYIQLVGMRLGIAAGM 734
Db 659 GQPDHPVILHEGVVKTSPVMIITEFMENGSLDSFLRQNDQGFYIQLVGMRLGIAAGM 718
QY 735 KYLDADNYVHRDLAARNILVNSNLVCKVSDPGLSRFLEDDTSDPTYTSLAGGKIPRWTA 794
Db 719 KYLDADNYVHRDLAARNILVNSNLVCKVSDPGLSRFLEDDTSDPTYTSLAGGKIPRWTA 778
QY 795 PEAIQYRKFTSASDVMSYGIYVMEVMSYGERPYWMDTNQDVINAIQDYRLPPMDCPSA 854
Db 779 PEAIQYRKFTSASDVMSYGIYVMEVMSYGERPYWMDTNQDVINAIQDYRLPPMDCPSA 838
QY 855 LHQJMLDCWQKDRNHRPKFGQIVNLDKXIRNPNLSIKAMAPLSSGINPLDRTIPDYTS 914
Db 839 LHQJMLDCWQKDRNHRPKFGQIVNLDKXIRNPNLSIKAMAPLSSGINPLDRTIPDYTS 898
QY 915 FNTVDEWLEAIKMGQYKESFANAGFTSPVVSOMMEDILRYGVTLAGHOKKILNSIQVM 974
Db 899 FNTVDEWLEAIKMGQYKESFANAGFTSPVVSOMMEDILRYGVTLAGHOKKILNSIQVM 958
QY 975 RAQMNQIQSYVE 985
Db 959 RAQMNQIQSYVE 969

Search completed: August 28, 2004, 04:15:01
Job time : 25.8114 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2004, 04:08:55 ; Search time 67.1975 Seconds
(without alignments)
4939.422 Million cell updates/sec

Title: US-09-914-883-4
Perfect score: 5571
Sequence: 1 MALRRLGALLLLPLLAAYE.....QGIFPKDSKESNDCSCG 1055

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues
Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 90%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications_AA.*
1: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/prodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/prodata/2/pubpaa/US09C_NEW_PUB.pep:*
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18: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5571	100.0	1055	16	US-10-648-593-139 Sequence 139, App
2	5170.5	92.8	987	15	US-10-295-027-1193 Sequence 1193, App

ALIGNMENTS

TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
FILE REFERENCE: D0273 NP
CURRENT APPLICATION NUMBER: US/10/648,593
CURRENT FILING DATE: 2003-08-26
PRIOR APPLICATION NUMBER: 60/406,385
PRIOR FILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 557
SOFTWARE: PatentIn version 3.2
SEQ ID NO 139
LENGTH: 1055
TYPE: PRT
ORGANISM: Homo sapiens
US-10-648-593-139

Query Match 100.0%; Score 5571; DB 16; Length 1055;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1055; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MALRRLGALLLLPLLAAYEETLMDSTTATLGMVHPSPGWEVSGYDENNTIRTYQ	60
DB	1	MALRRLGALLLLPLLAAYEETLMDSTTATLGMVHPSPGWEVSGYDENNTIRTYQ	60
QY	61	VGNVFESSQNNWLRKFIIRRGARHIVHVKAFSVDCSSISVPSGCKETNLYYEADF	120
DB	61	VGNVFESSQNNWLRKFIIRRGARHIVHVKAFSVDCSSISVPSGCKETNLYYEADF	120
QY	121	DSATKTFPNNMNPVVKYDTIAADESPQVDLGRVVKINTREVSFGVSSGFYLAQD	180
DB	121	DSATKTFPNNMNPVVKYDTIAADESPQVDLGRVVKINTREVSFGVSSGFYLAQD	180
QY	181	YGGCNSLIAYVFRKCRRIIIONGAIFOETLSGAEISTLVARSGCIANAEEVDVPIYX	240
DB	181	YGGCNSLIAYVFRKCRRIIIONGAIFOETLSGAEISTLVARSGCIANAEEVDVPIYX	240
QY	241	CNGDEMLVPIGRGCMCKAFEAVENTGRCGPGSTFPANGDEACTHCPINSRTTSGA	300
DB	241	CNGDEMLVPIGRGCMCKAFEAVENTGRCGPGSTFPANGDEACTHCPINSRTTSGA	300
QY	301	TNCVCRNGYRADDPLDMPCTTIPSAPOAVISSVNEISLMEWTPPRDSGREDLYNI	360
DB	301	TNCVCRNGYRADDPLDMPCTTIPSAPOAVISSVNEISLMEWTPPRDSGREDLYNI	360
QY	361	ICKSGSGRGACTRGDNVQYARPOLGLTEPRITYSDLLATQVTFEIOANGVTDOSPF	420
DB	361	ICKSGSGRGACTRGDNVQYARPOLGLTEPRITYSDLLATQVTFEIOANGVTDOSPF	420
QY	421	SPQFASVNTTNOAPASAVSIMHGVSRVDSITLSWSQPDOPNGVILDELYQYEKELSE	480
DB	421	SPQFASVNTTNOAPASAVSIMHGVSRVDSITLSWSQPDOPNGVILDELYQYEKELSE	480
QY	481	YNATAIKSPNTVTYOGAKAGIYFYQYRARTVAGYGSGMTFQMTAEYQTSIEK	540
DB	481	YNATAIKSPNTVTYOGAKAGIYFYQYRARTVAGYGSGMTFQMTAEYQTSIEK	540
QY	541	LPLITGSSAAGLVFLIAVVVAIVCNRRGFERRASEYTDKLOHTSGMTEGMKIYIDPF	600
DB	541	LPLITGSSAAGLVFLIAVVVAIVCNRRGFERRASEYTDKLOHTSGMTEGMKIYIDPF	600
QY	601	TYEDPNEAVREPAKEDIDSCVKEIOVIGAGEFGEVCSGHLKPKGREIFVAIKTLKSGYT	660
DB	601	TYEDPNEAVREPAKEDIDSCVKEIOVIGAGEFGEVCSGHLKPKGREIFVAIKTLKSGYT	660
QY	661	EKQRDPFISEASIMQCPHPNVTHLEGVYTKSTPMIITEEMENSGIDSPRONDGQFTV	720
DB	661	EKQRDPFISEASIMQCPHPNVTHLEGVYTKSTPMIITEEMENSGIDSPRONDGQFTV	720
QY	721	IQVGMGLGIAAGMYLADNMVYHRDLAARNILVNSNLVCKVSPGLSRFLEDITSDPTV	780
DB	721	IQVGMGLGIAAGMYLADNMVYHRDLAARNILVNSNLVCKVSPGLSRFLEDITSDPTV	780
QY	781	TSALGKPIPIRTAEALQYRFTSASDVWSYGIYMEVMSYGERPPYDMNTQVYINAE	840
DB	781	TSALGKPIPIRTAEALQYRFTSASDVWSYGIYMEVMSYGERPPYDMNTQVYINAE	840

QY 841 QDYRLPPMDCPSALHQLMLDCWQKDNHRPKFGQIVNTLDMKIRNPNSLKAMAPLSSG 900
Db 841 QDYRLPPMDCPSALHQLMLDCWQKDNHRPKFGQIVNTLDMKIRNPNSLKAMAPLSSG 900
QY 901 NLPLDLRTIPDYTSFNTVDWMLKAIKMGQYKESFANAGFTSPDVQOMMEDILRAGVTL 960
Db 901 NLPLDLRTIPDYTSFNTVDWMLKAIKMGQYKESFANAGFTSPDVQOMMEDILRAGVTL 960
QY 961 AGHQKXILNSIQVRAQMNQIQSVGQPLARRPRATGRTKRCOPRVYTKTCKNSNDGKK 1020
Db 961 AGHQKXILNSIQVRAQMNQIQSVGQPLARRPRATGRTKRCOPRVYTKTCKNSNDGKK 1020
QY 1021 GMGKKTDPGRGREIQGIFKEDSHKESNDSCGG 1055
Db 1021 GMGKKTDPGRGREIQGIFKEDSHKESNDSCGG 1055

RESULT 2
US-10-295-027-1193
Sequence 1193, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afari, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynn, Richard
APPLICANT: Hevez, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Marley, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1193
LENGTH: 987
TYPE: PRT
ORGANISM: Homo sapiens
US-10-295-027-1193

Query Match 92.8%; Score 5170.5; DB 15; Length 987;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 984; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
1 MALRRLGAAALLPLLAAVEETLMDSTTATLAEIWMVHPSPGWEVSGYDENMTIRTYQ 60

Db 1 MALRRLGAAALLPLLAAVEETLMDSTTATLAEIWMVHPSPGWEVSGYDENMTIRTYQ 60
QY 61 VCNVPESSQNNWLTATKPIRRRGARHIVEMKESVRDQSGSIPSVGSCKEFTNLYYADP 120
Db 61 VCNVPESSQNNWLTATKPIRRRGARHIVEMKESVRDQSGSIPSVGSCKEFTNLYYADP 120
QY 121 DSATKTFPNNMENNPMVKVDTIAADESFSQVLDGGRWVKINTEVSSFGVRSRSGYLAFO 180
Db 121 DSATKTFPNNMENNPMVKVDTIAADESFSQVLDGGRWVKINTEVSSFGVRSRSGYLAFO 180
QY 181 YGGCMSLIAVAFYKRCPRITQNGAIFQETLSGAESTSLVAARSGCIANAEDVPIKLY 240
Db 181 YGGCMSLIAVAFYKRCPRITQNGAIFQETLSGAESTSLVAARSGCIANAEDVPIKLY 240
QY 241 CNGGEMVLPVIGRCMCKAGFEAVENGTVCGCPGSGTKRANQGDPACTHCPINRTSEGA 300
Db 241 CNGGEMVLPVIGRCMCKAGFEAVENGTVCGCPGSGTKRANQGDPACTHCPINRTSEGA 300
QY 301 TNCVCRNGYRADDPLDMPCTTIPSAPOAVISSVNETSMLMTWTPRDSGGREDLVYNI 360
Db 301 TNCVCRNGYRADDPLDMPCTTIPSAPOAVISSVNETSMLMTWTPRDSGGREDLVYNI 360
QY 361 ICKSGSGRGACTCGGNVQAPARQGLTEPRITVYISDLIAHTQYTFEIQAVNGVTDQSP 420
Db 361 ICKSGSGRGACTCGGNVQAPARQGLTEPRITVYISDLIAHTQYTFEIQAVNGVTDQSP 420
QY 421 SPOFASVNTTNOAPASVNSIMQVSRVDSITLSWSQPDQPNGVILDELYOYKELSE 480
Db 421 SPOFASVNTTNOAPASVNSIMQVSRVDSITLSWSQPDQPNGVILDELYOYKELSE 480
QY 481 YNATAIKSPTNTVVOGLKAGAIYFQVRAATVAGYRSGKMYFOQMTAEVQTSIQEK 540
Db 481 YNATAIKSPTNTVVOGLKAGAIYFQVRAATVAGYRSGKMYFOQMTAEVQTSIQEK 540
QY 541 LPLIIGSSAAGVPLVAVVIAVCNRRFERADSEYTKLOHYSNGHMPGKIYIDP 599
Db 541 LPLIIGSSAAGVPLVAVVIAVCNRRFERADSEYTKLOHYSNGHMPGKIYIDP 599
QY 600 FTYEDPNEAVREPKAEIDISCKTEQYIAGGEFGEVSCGHLKPKGRKEIVAIKTLKSGY 659
Db 600 FTYEDPNEAVREPKAEIDISCKTEQYIAGGEFGEVSCGHLKPKGRKEIVAIKTLKSGY 659
QY 661 FTYEDPNEAVREPKAEIDISCKTEQYIAGGEFGEVSCGHLKPKGRKEIVAIKTLKSGY 660
Db 661 FTYEDPNEAVREPKAEIDISCKTEQYIAGGEFGEVSCGHLKPKGRKEIVAIKTLKSGY 660
QY 720 VIQVGMRLGIAAGKYLADNYYHRDLAARNILVNSNLVCKVSDFGLSRFLDDTSDPT 780
Db 720 VIQVGMRLGIAAGKYLADNYYHRDLAARNILVNSNLVCKVSDFGLSRFLDDTSDPT 780
QY 780 YTSALGKIPRMTAPPAIQYRKFTSADVWSGIWMEVMSYGERPYWMTNODVYNAI 839
Db 780 YTSALGKIPRMTAPPAIQYRKFTSADVWSGIWMEVMSYGERPYWMTNODVYNAI 839
QY 840 EODYRLPPMDCPSALHQLMLDCWQKDNHRPKFGQIVNTLDMKIRNPNSLKAMAPLSSG 899
Db 840 EODYRLPPMDCPSALHQLMLDCWQKDNHRPKFGQIVNTLDMKIRNPNSLKAMAPLSSG 899
QY 900 INPLDLRTIPDYTSFNTVDWMLKAIKMGQYKESFANAGFTSPDVQOMMEDILRAGV 959
Db 900 INPLDLRTIPDYTSFNTVDWMLKAIKMGQYKESFANAGFTSPDVQOMMEDILRAGV 959
QY 960 LAGHQKXILNSIQVRAQMNQIQSVG 985
Db 960 LAGHQKXILNSIQVRAQMNQIQSVG 986

Search completed: August 28, 2004, 04:17:15
Job time : 68.1975 secs